



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 168824

TO: Celine Qian
Location: rem/2A64/2C70
Art Unit: 1636
Monday, May 15, 2006
Case Serial Number: 09/921143

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: (571)272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Qian,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2523



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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact:*

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



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CRAFT

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: Celine Qian Examiner # 78710 Date: 5/4/06
Art Unit: 1636 Phone Number: 2-0777 Serial Number: 091921143
Location (Bldg/Room#): 2A64 (Mailbox #): 2670 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following: ME

Title of Invention: Vascular endothelial growth factor-2

Inventors (please provide full names): Coleman, T.

Earliest Priority Date: 8/3/2000

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO:36 (both commercial & interference database).

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	____ NA Sequence (#)	____ STN ____ Dialog
Searcher Phone #: _____	____ AA Sequence (#)	____ Questel/Orbit ____ Lexis/Nexis
Searcher Location: _____	____ Structure (#)	____ Westlaw ____ WWW/Internet
Date Searcher Picked Up: _____	____ Bibliographic	____ In-house sequence systems
Date Completed: _____	____ Litigation	____ Commercial ____ Oligomer ____ Score/Length
Searcher Prep & Review Time: _____	____ Fulltext	____ Interference ____ SPDI ____ Encode/Transl
Online Time: _____	____ Other	____ Other (specify)

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2006, 17:29:01 ; Search time 17095 Seconds
(without alignments)
17566.771 Million cell updates/sec

Title: US-09-921-143-36

Perfect score: 5283

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:.*
1: gb_ba:.*
2: gb_in:.*
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4: gb_om:.*
5: gb_cv:.*
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7: gb_ph:.*
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14: gb_hcg:.*
15: gb_pl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2312.6	43.8	8786	11	AY622810
3	2309.6	43.7	9816	11	AY622811
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6	2218.4	42.0	2999	11	SYNCCDBA
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10	2177.4	41.2	11403	11	AY189829
11	2088.4	39.5	3036	11	AY222815
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C 38	1603.8	30.4	3534	6	CQ854727	CQ854727 Sequence
C 39	1603.8	30.4	3534	6	CQ854741	CQ854741 Sequence
C 40	1603.8	30.4	3534	6	CQ903781	CQ903781 Sequence
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C 45	1603.8	30.4	3534	6	CS131823	CS131823 Sequence

ALIGNMENTS

RESULT 1
LOCUS CVE18316
DEFINITION Cloning vector pKGM.
ACCESSION Y18316
VERSION Y18316.1 GI:5830187
KEYWORDS bleomycin resistance; cloning vector; kanamycin resistance;
multiple cloning site; neomycin resistance.
SOURCE Cloning vector pKGM
ORGANISM Bannasch, D.
REFERENCE 1
AUTHORS Bannasch, D. and Schwab, M.
TITLE A versatile bait vector for rapid Gal4 dependent two-hybrid screens
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6074)
AUTHORS Bannasch, D.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1998) D. Bannasch, Institution Division of,
Cytogenetics/H0400 Deutsches, Krebsforschungszentrum (DKFZ), Im
Neuenheimer Feld 280, D-69120 Heidelberg, FRG
REMARK Revised by author 10-JUN-1999
COMMENT Related sequences U07646, U00004, L19385.
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Db 1954 CGTAATCATGTCATAGCTGTTTCTGTGTGAATTTGTTATCCGCTCACAAATTCACACA 2013
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Db 2014 ACATAGAGCCGGAAGCATTAAGTGTAAAGCTGGGGTGCTTATGATGAGCTAACTCA 2073
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Db 2074 CATTAAATGCGTTGGCGTCACTGCGCGCTTTCAGATCGGGAACCTGTGTCAGCTG 2133
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DEFINITION	Cloning shuttle vector pSCB119, complete sequence.		
ACCESSION	AY622810		circular SYN 14-MAR-2005

	VERSION	AY622810.1	GI:60651293
	KEYWORDS		
	SOURCE	Cloning shuttle vector pSCR119	
	ORGANISM	Cloning shuttle vector pSCR119 other sequences; artificial sequences; vectors.	
	REFERENCE	1 (bases 1 to 8786) Summers,M.L., Wallis,J.G., Campbell,E.L. and Meeks,J.C. Genetic evidence of a major role for glucose-6-phosphate dehydrogenase in nitrogen fixation and dark growth of the cyanobacterium Nostoc sp. strain ATCC 29133	
	AUTHORS	J.J. Bacteriol. 177 (21), 6184-6194 (1995)	
	TITLE	75923184	
	JOURNAL	2 (bases 1 to 8786) Argüeta,C., Yukeek,K. and Summers,M. Construction and use of GFP reporter vectors for analysis of cell-type-specific gene expression in Nostoc punctiforme J. Microbiol. Methods 59 (2), 181-188 (2004)	
	PUBMED	15369854	
	REFERENCES	3 (bases 1 to 8786) Summers,M.L., Wallis,J.G., Campbell,E.L. and Meeks,J.C. Submitted (08-MAY-2004) Biology, CSU Northridge, 18111 Nordhoff St., Northridge, CA 91330-8303, USA	
	AUTHORS	Location/Qualifiers	
	JOURNAL	1..8786	
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	ORIGIN		
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	Best Local Similarity	92.1%; Pred. No. 0;	
	Matches 2490; Conservative	0; Mismatches 144; Indels 71; Gaps 2;	
Dy	2650	GCGAACATGAGTGCGCTGCCTGAGAGTGTGCGGCTTAATCATCTGACAGCTGTCTAG	27099
Dd	210	GTGAATTGAGCTCGTTACCCTGGGAGTCCCTTAGAGTCGACTGACAGCATGCAAGCTTG	269
Oy	2710	ACGTATCATGCTCATAGCTGTTTCTCTGTGTGAATTGTTATCCGCTCACATTCACAC	2769

Db	270	GGGTATATATGGTCACTAGCTGTTTCTCTGTGTGAATTTGTTATCCGCTCACAATTCCAC	329
QY	2770	AACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTTAATGATGAGCTAACTC	2822
Db	330	AAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTTAATGATGAGCTAACTC	389
QY	2830	ACATTAAATGGGTGAGCTCACTGCGCGCTTCCAGTGGGGAACCTGTCTGCGCAAGCTG	2885
Db	330	ACATTAAATGGGTGAGCTCACTGCGCGCTTCCAGTGGGGAACCTGTCTGCGCAAGCTG	449
QY	2890	CATTATGAAATCGGCAACCGCGGGGAGAGGCGGTGTGCGTATTTGGGCGCTCTCCGCT	2945
Db	450	CATTATGAAATCGGCAACCGCGGGGAGAGGCGGTGTGCGTATTTGGGCGCTCTCCGCT	509
QY	2950	TCCTCGCTCACTGAGTCCGTGGCTGGCTCGTTCGCTGCGCGCGCGGTATCACTCAAC	3005
Db	510	TCCTCGCTCACTGAGTCCGTGGCTGGCTCGTTCGCTGCGCGCGCGGTATCACTCAAC	569
QY	3010	TCAAAAGCGGTAAATACGCGTTATCCACAGAAATAGGGGATTAACGACGAAAGAACATGTGA	3065
Db	570	TCAAAAGCGGTAAATACGCGTTATCCACAGAAATAGGGGATTAACGACGAAAGAACATGTGA	629
QY	3070	GCAAAAGGCGACGCAAAAAGCCAGAACCGTAAANAAGCCGCGTTGCTGCGTTTTCCAT	3125
Db	630	GCAAAAGGCGACGCAAAAAGGCGACGAAACCGTAAANAAGGCGCGCTGCTGCGTTTTCCAT	689
QY	3130	AGGCTCGCGCCCCCTGAGAGAGATCAAAAATGCAAGCTCAAGTCANAGGTGGGGAAC	3185
Db	690	AGGCTCGCGCCCCCTGAGAGAGATCAAAAATGCAAGCTCAAGTCANAGGTGGGGAAC	749
QY	3190	CCGACAGGACTATAAAGATATACAGGCGTTTTCCCTCGAGAGCTCCCTCGTGGCGCTCCT	3245
Db	750	CCGACAGGACTATAAAGATATACAGGCGTTTTCCCTCGAGAGCTCCCTCGTGGCGCTCCT	809
QY	3250	GTTCCGACCCCTGCGGCTTAACCGGAATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCG	3305
Db	810	GTTCCGACCCCTGCGGCTTAACCGGAATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCG	869
QY	3310	CTTTCTCACTACCTGACGCTGTAGGTATCTAGTTGGGTAGGTGTTGCTCCCAAGCTG	3365
Db	870	CTTTCTCACTACCTGACGCTGTAGGTATCTAGTTGGGTAGGTGTTGCTCCCAAGCTG	929
QY	3370	GGCTGTGTGACGAAACCCCGGTTCAAGCCGACCGCTGGCGCTTATCCGGTAACTATCGT	3425
Db	930	GGCTGTGTGACGAAACCCCGGTTCAAGCCGACCGCTGGCGCTTATCCGGTAACTATCGT	989
QY	3430	CTTAGAGTCCAACCCGGTAAAGACAGACTTATCGGCACTGGGACGACGCACTGGTAAACAG	3485
Db	990	CTTAGAGTCCAACCCGGTAAAGACAGACTTATCGGCACTGGGACGACGCACTGGTAAACAG	1049
QY	3490	ATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGATTTCTTGAAGTGTGGCTTAACAC	3545
Db	1050	ATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGATTTCTTGAAGTGTGGCTTAACAC	1109
QY	3550	GGCTACACTAAGAAACAGATTTTGTATCTAGCGCTGCTGGAAGCAAGTAACTTCCGGA	3609
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QY	3610	AAAAGAGTGTAGCTCTTGATCCGGCAAAACACACGCTGGTAGCGGTGTTTTTTT	3665
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QY	3730	TCTAACGGGGTCTGACGCTCACTGGAACGAAAACTCAGCTTAAAGGAATTTTGGTCATGGA	3785
Db	1290	TCTAACGGGGTCTGACGCTCACTGGAACGAAAACTCAGCTTAAAGGAATTTTGGTCATGGA	1345
QY	3790	TTTATCTGTCACCA-----	3802
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QY	3803	-----AAGCCGCATCGTGGCTCCCACTCTCTGCAGTTCCGGGGCATG	384
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Db	1470	ATCTCAGGATCTGTCTATTTCTGTTCAATCCATAGTGTCTACCTCCCGTGTGTAGATA	1522
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Db	1650	CGGGCTCCCGGAAACGATTCGAAAGCCCACTTTCAATAGAGCGCGGGTGAATCGA	1709
QY	4079	AATCTCGATAGGAGGTGGGGCGTCCGCTGGTGTGCATTTGCAACCCGAGTCCCGC	4138
Db	1710	AATCTCGATAGGAGGTGGGGCGTCCGCTGGTGTGCATTTGCAACCCGAGTCCCGC	1765
QY	4139	TCAGAGAACTCTCAAGAAAGCCATAGAAAGCCATGCGCTGCATTCGAGAGCGCGAT	4198
Db	1770	TCAGAGAACTCTCAAGAAAGCCATAGAAAGCCATGCGCTGCATTCGAGAGCGCGAT	1829
QY	4199	ACCGTAAAGCACGAGAAAGCGGTACGCCATATCCCGCGCAAGCTTTCAAGCAATACG	4258
Db	1830	ACCGTAAAGCACGAGAAAGCGGTACGCCATATCCCGCGCAAGCTTTCAAGCAATACG	1889
QY	4259	GGTAGCCACGCTATGTCTGTATGCGAGTCCGGCACACCCGCGGCGACAGTGATGAA	4318
Db	1890	GGTAGCCACGCTATGTCTGTATGCGAGTCCGGCACACCCGCGGCGACAGTGATGAA	1949
QY	4319	TCGAGAAAGCGGCATATTTTCACCATGATATTCGCGAAGCGGCATCGCCATGGGTAC	4378
Db	1950	TCGAGAAAGCGGCATATTTTCACCATGATATTCGCGAAGCGGCATCGCCATGGGTAC	2009
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RESULT 4
AR260588
LOCUS AR260588 8349 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 16 from patent US 6489542.
ACCESSION AR260588
VERSION AR260588.1 GI:27311143
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8349)
AUTHORS Corbin, D. R. and Romano, C. P.
TITLE Methode for transforming plants to express Cry2Ab
JOURNAL .delta.-endotoxins targeted to the plastids
Patent: US 6489542-A 16 03-DEC-2002;
Monsanto Technology LLC, St. Louis, MO
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location/Qualifiers
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/mol_type="genomic DNA"
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Query Match 42.4%; Score 2240; DB 6; Length 8349;
Best Local Similarity 93.4%; Pred. No. 0; Mismatches 25; Indels 144; Gaps 1;
Matches 2409; Conservative 0; Mismatches 25; Indels 144; Gaps 1;
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QY 2766 ACACAACTATGAGCCGGAACATTAAGTGAAGCTGGGGTGCCTAATAGTAGCTA 2825
Db 5971 ACACAACTATGAGCCGGAACATTAAGTGAAGCTGGGGTGCCTAATAGTAGCTA 6030
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QY	5226	TTCTACGCTGTCCGCGCTTCCTTTACAGCGCCCTTGCGGCGTGGAGTCTTGGCGGACAGCG	5283
Db	8287	TTCTACGCTGTCCGCGCTTCCTTTACAGCGCCCTTGCGGCGTGGAGTCTTGGCGGACAGCG	8344
RESULT 5			
SYN8MRGC/c			
LOCUS	SYN8MRGC	2661 bp	DNA linear SYN 27-APR-1993
DEFINITION	Synthetic plasmid pK18 (pBRneo/pUC18) Kanamycin resistance gene, complete cde.		
ACCESSION	MI7626	MI7626.1	GI:207845
VERSION	complete genome; kanamycin resistance.		
KEYWORDS	unidentified cloning vector		
SOURCE	unidentified cloning vector		
ORGANISM	other sequences; artificial sequences; vectors.		
REFERENCE	1 (bases 1 to 2661)		
AUTHORS	Pridmore,R.D.		
TITLE	New and versatile cloning vectors with kanamycin-resistance marker		
JOURNAL	Gene 56 (2-3), 309-312 (1987)		
PUBMED	331864		
COMMENT	Original source text: Plasmid pBRneo and pUC18 DNA.		
FEATURES	Location/Qualifiers		
source	1..2661		

[illegible]

Db 1543 AAAGATTGGTACTCTTGATCCGGCAAAACAACCGCTGTAGCCGTGGATTTTGTG 1484
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Db 1483 TTTCGACGACAGATTACGCGCAGAAAAAAGATCTCAAGAAGATCTTTGATCTTTT 1424
Qy 3731 CTACGGGGTCTGACGCTCAGTGGAAAGAAAACTCAGTTAAGGATTTTGGTCAATGAT 3790
Db 1423 CTACGGGGTCTGACGCTCAGTGGAAAGAAAACTCAGTTAAGGATTTTGGTCAATGAT 1364
Qy 3791 TATGTCGACCAAAAGCGGCATTCGTCTCCCACTCTCGAATTCGGGGCAGTGAATC 3850
Db 1363 TATCAAAAAGATCTTCACTGAGATCTT----- 1335
Qy 3851 GCGGATAGCCGCTGCTGGTTCTTGATGCCAGCGGATTTGCACTGCCGATGAACCTCG 3910
Db 1334 ----- 1335
Qy 3911 CGAGGTGCTCCAGCTTCAGGAGAGCTGAACCACTCGAGGGGATCGAGCCCGGGT 3970
Db 1334 -----TTGGGGT 1328
Qy 3971 GGGGGAAGAACTCCAGCATGAGATCCCGCGCTGAGGATCATCGCCGCGTCCGGA 4030
Db 1327 GGGGGAAGAACTCCAGCATGAGATCCCGCGCTGAGGATCATCGCCGCGTCCGGA 1268
Qy 4031 AAAGCATTCGGAAGCCCACTTTCATGAAAGGGGGGTGGAATCGAATCTGTGATG 4090
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Db 1207 GCAGGTGGGGGTGCTTGGTCCGTCATTTGAAACCCAGAGTCCCGTCCAGAAATC 1148
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Db 1147 GTCAAGAGGAGATGAAAGGGGATCGCTGCAATTCGGAAGCGCGGATACCTGAAAGAC 1088
Qy 4211 GAGGAGCGGTCAGCCCATTCGCGCCAGAGCTTTCAGCAATTCAGGGGTAGGCAAGC 4270
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Qy 4271 TATGTCCTGATAGCGGTCCGCAACCCAGCGGCAAGTCGATGATCCAGAAAGCG 4330
Db 1027 TATGTCCTGATAGCGGTCCGCAACCCAGCGGCAAGTCGATGATCCAGAAAGCG 968
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Db 967 GCCATTTTCCACCTGATATTCGGAAGAGGATCGCCATGGGTCAAGAGATCTTC 908
Qy 4391 GCGGTGGGGATGGCGGCTTGAAGCTGGGGAAGTTCCGCTGGCGCGAGCCCTGATG 4450
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Qy 4451 CTCTTCCTCAGATCATCTGATGCAAGACCGGCTTCCATCCGATACGTGCTCCCTC 4510
Db 847 CTCTTCCTCAGATCATCTGATGCAAGACCGGCTTCCATCCGATACGTGCTCCCTC 788
Qy 4511 GATGCGATTTTTCGCTTGGTGGTGAATGGCAGGTAGCCGGATCAAGCGTATGACCGG 4570
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Qy 4571 CCGGATTCGATCAGCCATGATGATCTTTCTCGGCGAGGAGCAAGTGAATGACAGAG 4630
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Qy 4631 ATCTGCGCCGCGCATTCGCGCAATAGCAGGACGCTTCCGCTTCAAGTCAAGAGTC 4690
Db 667 ATCTGCGCCGCGCATTCGCGCAATAGCAGGACGCTTCCGCTTCAAGTCAAGAGTC 608
Qy 4691 GAGGACAGCTGCGGAAGAAAGCCCGTCTGGGCGAGCAAGATGCGCGCTGCTGTC 4750
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Qy 4811 CGTGAAGCCGGAACAAGCGGCGATCAGACACCGATTTGTCTGTGGCCAGTCATA 4870
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Qy 4871 GCCGAATAGCTCTTCACCCAGAGCGCGGAGAACTGCGTGCATTCATTTGTTCAAT 4930
Db 427 GCCGAATAGCTCTTCACCCAGAGCGCGGAGAACTGCGTGCATTCATTTGTTCAAT 368
Qy 4931 CATGCAAGAGATCTCATCTGCTCTTGAATGATCTTGAATCCCTCGGCGCATTCAGAT 4990
Db 367 CATGCAAGAGATCTCATCTGCTCTTGAATGATCTTGAATCCCTCGGCGCATTCAGAT 308
Qy 4991 CTTGGCGGCAAGAAAGCCATTCAGTTTACTTTGACAGGGCTTCCCACTTACAGAGGG 5050
Db 307 CTTGGCGGCAAGAAAGCCATTCAGTTTACTTTGACAGGGCTTCCCACTTACAGAGGG 248
Qy 5051 GCGCCAGCTGGCAATTCGCGTTCGTTGCTGTCATTAACCGCCAGTCTAGCTATCG 5110
Db 247 GCGCCAGCTGGCAATTCGCGTTCGTTGCTGTCATTAACCGCCAGTCTAGCTATCG 188
Qy 5111 CCATGTAAGCCACTGCAAGCTACCTGCTTCTCTTGGCGTTGGCGTTTCCCTTGTCCA 5170
Db 187 CCATGTAAGCCACTGCAAGCTACCTGCTTCTCTTGGCGTTGGCGTTTCCCTTGTCCA 128
Qy 5171 GATAGCCAGTAGCTGATTCATTCGCGGGTCAGACCGTTTTCGCGAGCTGCTTCTA 5230
Db 127 GATAGCCAGTAGCTGATTCATTCGCGGGTCAGACCGTTTTCGCGAGCTGCTTCTA 68
Qy 5231 CGTGTCCGCTTCTTTAGACGCCCTTGGCGCCTGAGTGTCTTGGCGAGCGTGT 5283
Db 67 CGTGTCCGCTTCTTTAGACGCCCTTGGCGCCTGAGTGTCTTGGCGAGCGTGT 15

RESULT 6
SYNCDDB/c 2999 bp DNA linear SYN 16-MAR-2000
LOCUS
DEFINITION
Cloning vector pKil118 ccdB gene, complete cds and
kanamycin-resistance (Kmr) gene fragment.
138498
ACCESSION
U38498.1 GI:986977
VERSION
ccdB gene; cloning vector; kanamycin resistance.
KEYWORDS
Cloning vector pKil118
SOURCE
Cloning vector pKil118
ORGANISM
other sequences; artificial sequences; vectors.
REFERENCE
1. (bases 1 to 2999)
AUTHORS
Bernard, P.
TITLES
New ccdB positive-selection cloning vectors with kanamycin or
chloramphenicol selectable markers
JOURNAL
Gene 162 (1), 159-160 (1995)
PUBMED
7557407
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ORIGIN

Query Match 42.0%; Score 2218.4; DB 11; Length 2999;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 2388; Conservative 0; Mismatches 26; Indels 144; Gaps 1;

QY 2726 AGCGTGTCTCTGTGTAATTTGTTATCCGCTCAATTCACACATATGAGCCGAA 2785
DB 2999 AGCTGTTCTCTGTGTAAATTTGTTATCCGCTCAATTCACACATATGAGCCGAA 2940
QY 2786 GCATTAAGTAAAGCTGGGGTGCCTAATAGTGAAGTAACTCACTTAATTCGTTGC 2845
DB 2939 GCATTAAGTAAAGCTGGGGTGCCTAATAGTGAAGTAACTCACTTAATTCGTTGC 2880
QY 2846 GCTACATGCCCCCTTCCAGTCGGGAAACCTGTCTGSCGAGCTGACATTAATGAGGCC 2905
DB 2879 GCTACATGCCCCCTTCCAGTCGGGAAACCTGTCTGSCGAGCTGACATTAATGAGGCC 2820
QY 2906 AAGCGCGGGGAGAGCGGTTTGCGTATTTGGGCGCTTTCGCGTCTCTGCTCACTGACT 2965
DB 2819 AAGCGCGGGGAGAGCGGTTTGCGTATTTGGGCGCTTTCGCGTCTCTGCTCACTGACT 2760
QY 2966 CGCTGCGCTCGGTCTGCTGCGCTGCGCGAGCGGTATCACTCACTCAAGCGGTAAATAC 3025
DB 2759 CGCTGCGCTCGGTCTGCTGCGCTGCGCGAGCGGTATCACTCACTCAAGCGGTAAATAC 2700
QY 3026 GGTATTCACAGATCAGGGGATPAAGCAGAGAAACATGTGAGCAAAAGCGCAGAA 3085
DB 2699 GGTATTCACAGATCAGGGGATPAAGCAGAGAAACATGTGAGCAAAAGCGCAGAA 2640
QY 3086 AGGCGAGGAACCGTAAAGAGCGCGCTTGCTGGCTTTTTCATAGGCTCCGCCCCCTG 3145
DB 2639 AGGCGAGGAACCGTAAAGAGCGCGCTTGCTGGCTTTTTCATAGGCTCCGCCCCCTG 2580
QY 3146 ACCAGACTCACAAAATTCGACGCTCAAGTCAAGGTGGCGAAACCGCAGACGACTATAA 3205
DB 2579 ACCAGACTCACAAAATTCGACGCTCAAGTCAAGGTGGCGAAACCGCAGACGACTATAA 2520
QY 3206 GATACAGGCGTTTCCCCCTGGAAGCTCCCTGCGGCTCCCTGTTCCGACCCCTGCGC 3265
DB 2519 GATACAGGCGTTTCCCCCTGGAAGCTCCCTGCGGCTCCCTGTTCCGACCCCTGCGC 2460
QY 3266 TTACCGGATACCTGTCCGCTTTCTCCCTTCCGGAAGCGTGGCGCTTTCATAGCTCAC 3325
DB 2459 TTACCGGATACCTGTCCGCTTTCTCCCTTCCGGAAGCGTGGCGCTTTCATAGCTCAC 2400
QY 3326 GCTGTAGATATCTAAGTTCGGTGTAGGTGCTTCCCTCAAGCTGGGCTGTGTGACGAAC 3385
DB 2399 GCTGTAGATATCTAAGTTCGGTGTAGGTGCTTCCCTCAAGCTGGGCTGTGTGACGAAC 2340
QY 3386 CCCCCGTTACAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAATCCACCCG 3445
DB 2239 CCCCCGTTACAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAATCCACCCG 2280
QY 3446 TAAGACACGACTTATCGCACACTGCGACAGCACTGTGTAAACAGATTAGACAGAGGT 3505
DB 2279 TAAGACACGACTTATCGCACACTGCGACAGCACTGTGTAAACAGATTAGACAGAGGT 2220
QY 3506 ATGTAGCGGTGCTCAAGAGTCTTGAAGTGTGGCTTAACCTAAGCTTAACATAAGAA 3565
DB 2219 ATGTAGCGGTGCTCAAGAGTCTTGAAGTGTGGCTTAACCTAAGCTTAACATAAGAA 2160
QY 3566 CAGTATTGGTATCTGCGCTCTGCTGAAGCAAGTTACTTTCGAAAAAGAGTTGTAGCT 3625
DB 2159 CAGTATTGGTATCTGCGCTCTGCTGAAGCAAGTTACTTTCGAAAAAGAGTTGTAGCT 2100
QY 3626 CTTGATTCGGCAAAACAACACGCGCTGTAGCGGTGTTTTTTTTTTGTTGCAAGCAGAGA 3685
DB 2099 CTTGATTCGGCAAAACAACACGCGCTGTAGCGGTGTTTTTTTTTTGTTGCAAGCAGAGA 2040
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DB 2039 TTACGCGCAAAAAAAGAGTCTCAAGAGATCTTTTGAATCTTTTTCACGCGGTCTACG 1980
QY 3746 CTCAGTGAACGAAACCTCAAGTAAAGGATTTTGTGTCATGAGATTATCGTCGACCAAG 3805

DB 1979 CTCAGTGAACGAAACCTACACTTAAGGATTTTGTGCTATGAGATTATCAAAAAAGATCT 1920
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QY 3866 TGGTTTCTGATATGCCAGGATTTGCACTGCCGTAGAACTCCGAGGTGTCCAGCC 3925
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QY 3926 TCAGGACAGCTGAACCAACTCGGAGGGATCGAGCCCGGGTGGCGAAGAACTCCA 3985
DB 1905 -----TTGGGTGGGGAAGAACTCCA 1884
QY 3986 GCATGATATCCCGCGCTGAGAGATCATCAGCCGGCGCTCCCGAAAAAGATTCGAGC 4045
DB 1883 GCATGATATCCCGCGCTGAGAGATCATCAGCCGGCGCTCCCGAAAAAGATTCGAGC 1824
QY 4046 CCAACCTTTCATAGAAAGCGGGGTGGAATGGAATCTGTGATGGCAGGTTGGCGTGC 4105
DB 1823 CCAACCTTTCATAGAAAGCGGGGTGGAATGGAATCTGTGATGGCAGGTTGGCGTGC 1764
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DB 1763 CTTGGTCGCTCATTTTGAACCCCAAGATCCCGCTCAGAGAACTGTCAGAGAGCGATA 1704
QY 4166 GAAAGCGATCCGCTCGGAATCGGAGCGCGCATACCTGTAAACATCAGAGAACGCTCAC 4225
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DB 1463 CGCTTGAAGCTGCGCAACGTTTGGCTGGCGCAGACCCCTGATGCTCTTCTCCAGATC 1404
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DB 1403 ATCTGATGCAAGAACCGGCTTTCATTCGAGTACGTGCTGCTGATGCAATGTTGCG 1344
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QY 4706 AGGAAGCCCGCTGTGTGGCAGACAGATAGCCGCTGCTGTCTGTGAGATTCAATTGAG 4765
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QY 4766 GGCACCGGACAGGTGCTTTCAGCAAAAGAACCCGGCGCCCTTGTGCTGACGACCGGAA 4825
DB 1103 GGCACCGGACAGGTGCTTTCAGCAAAAGAACCCGGCGCCCTTGTGCTGACGACCGGAA 1044
QY 4826 CACGGCGGATCAGACAGCCGATTTGTCTGTTGTGCCAGTCAATGCGAATAGCTCTTC 4885

Db 1043 CAGGCGGATCAGACGCCGATGTCCTGTTGTCACAGTCATAGCCGAAATAGCCTCTC 984
Qy 4886 CACCCAGGCGGCGGAGAACTGCGTGAATCATCTTGTTCATCATGCGAAAGATCC 4945
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Qy 4946 TCATCTGCTCTTGTATGATGATCTTGTATCCCTGCGGCATGATCTTGGCGGAGAA 5005
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Db 743 GCAAGTACCTGCTTCTCTTGGCGCTTGCCTTTCCTTGTCCAGATAGCCAGTACT 684
Qy 5186 GACATTCATCCGGGCTCAGCACCTGTTTCTGCGAGCTGCTTCTAGGTTCCGCTTCT 5245
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Qy 5246 TTACAGGCTTGGCGCTGAGTGTGCTTGGCGAGCGTG 5283
Db 623 TTACAGGCTTGGCGCTGAGTGTGCTTGGCGAGCGTG 586

RESULT 7
SYNCCDB/c 2999 bp DNA linear SYN 16-MAR-2000
LOCUS Cloning vector pK1119 ccdB gene, complete cds and
DEFINITION kanamycin-resistance gene (km) gene fragment.
ACCESSION L38499.1 GI:986979
VERSION ccdB gene; kanamycin resistance.
KEYWORDS Cloning vector pK1119
SOURCE Cloning vector pK1119
ORGANISM Other sequences; artificial sequences; vectors.
REFERENCE 1 (bases 1 to 2999)
AUTHORS Bernard, P.
TITLE New ccdB positive-selection cloning vectors with kanamycin or
chloramphenicol selectable markers
JOURNAL Gene 162 (1), 159-160 (1995)
FEATURES
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ORIGIN

Query Match 42.0%; Score 2218.4; DB 11; Length 2999;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 2388; Conservative 0; Mismatches 26; Indels 144; Gaps 1;

Qy 2726 AGCTGTTCTCTGTGTAATTTGTTATCCGCTCACAATTCACACACATACGAGCGGAA 2785
Db 2999 AGCTGTTCTCTGTGTAATTTGTTATCCGCTCACAATTCACACACATACGAGCGGAA 2940

Qy 2786 GCATTAAGTGAAGCCCTGGGGTGCCTAATAGTAGCTAATCTCAATTAAATGGCTTC 2845
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Qy 2846 GCTCACTGCCCGCTTTCAGTCCGAGAAACCTGTGCTGCACTGATTAATGAATCGGCC 2905
Db 2879 GCTCACTGCCCGCTTTCAGTCCGAGAAACCTGTGCTGCACTGATTAATGAATCGGCC 2820
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Db 2819 AACCGCGGAGAAAGCGGCTTTCGTAATTGGGCGCTCTCCGCTTCTCGCTCACTGACT 2760
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Db 2699 GATTATCCACAGAAATCAGAGGATTAACGACGAAAGAAATGTAGAGCAAAAGGCGCAAA 2640
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Db 2639 AGCCAGAAACCGTAAAGGCGGCTTGTGCTGAGCTTTCATAGGCTCCGCCCTG 2580
Qy 3146 ACGAGCATCAAAAATCGACGCTCAAGTCAAGAGTGGCGCAAAACCGACAGACTATTA 3205
Db 2579 ACGAGCATCAAAAATCGACGCTCAAGTCAAGAGTGGCGCAAAACCGACAGACTATTA 2520
Qy 3206 GATACAGAGGCTTCCCGCTGAAAGCTCCCTGAGCGCTCCCTGTTCCGACCGCTGCGC 3265
Db 2519 GATACAGAGGCTTCCCGCTGAAAGCTCCCTGAGCGCTCCCTGTTCCGACCGCTGCGC 2460
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Db 2279 TAAGACACGACTATTCGCACTGCGACAGCACACTGGTAAACAGATTAGACAGACGAGT 2220
Qy 3506 ATGTAGCGGCTGCTACAGAGTCTTGAAGTGTGTGCTTAACTACGCTTACACTAGAA 3565
Db 2219 ATGTAGCGGCTGCTACAGAGTCTTGAAGTGTGTGCTTAACTACGCTTACACTAGAA 2160
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Db 1919 TCACCTAGATCCCTT----- 1906

QY 3866 TGGTTCCTGAGATCCGACGGATTTTGACTGCCGGTAGAACTCCGCGAGGTCGTCAGGCC 33925
Db 1905 ----- 1906
QY 3926 TCAGGACAGAGCTGAAACCACTCCGCGAGGGATTCAGCCCGGGGTGGGCGAAGAACTCCA 33985
Db 1905 -----TTGGGGTGGGCGAAGAACTCCA 1884
QY 3986 GCATAGATATCCCGCGCTGGAGATTCATTCAGCCGGCGGTCCCGGAAAAAGATTCGGAAGC 4045
Db 1883 GCATAGATATCCCGCGCTGGAGATTCATTCAGCCGGCGGTCCCGGAAAAAGATTCGGAAGC 1824
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QY 4166 GAAGGCGATGCGCTGCGCAATTCGGGAGCGGCGATTCGTTAAAGCAGAGAAAGCGGTACG 4225
Db 1703 GAAGGCGATGCGCTGCGCAATTCGGGAGCGGCGATTCGTTAAAGCAGAGAAAGCGGTACG 1644
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QY 4526 TTGCTGTGCAATGGGAGGATGCGCGATCAAGGTATGAGCGCCGCGATTGATCAGC 4585
Db 1343 TTGCTGTGCAATGGGAGGATGCGCGATCAAGGTATGAGCGCCGCGATTGATCAGC 1284
QY 4586 CATGATGATATCTTCTCGCAGAGCAAGTGAATCAGAGATCTGCCCCGCGAC 4645
Db 1283 CATGATGATATCTTCTCGCAGAGCAAGTGAATCAGAGATCTGCCCCGCGAC 1224
QY 4646 TTGCGCCCAATAGCAAGCCATTCCTTCGCTTCAAGTGAACAGTTCAGCAAGCTGCGCA 4705
Db 1223 TTGCGCCCAATAGCAAGCCATTCCTTCGCTTCAAGTGAACAGTTCAGCAAGCTGCGCA 1164
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ACCESSION AY189826
VERSION AY189826.1 GI:28435536
KEYWORDS
SOURCE
ORGANISM his-3 integration vector pUHAM01
his-3 integration vector pUHAM01
other sequences; artificial sequences; vectors.
REFERENCE
1 (bases 1 to 2604)
Lee,D.W., Haag,J.R. and Aramayo,R.
Construction of strains for rapid homokaryon purification after
integration of constructs at the histidine-3 (his-3) locus of
Neurospora crassa
CURR. GENET. 43 (1), 17-23 (2003)
JOURNAL
PUBMED 12684841
REFERENCE
2 (bases 1 to 2604)
Lee,D.W., Haag,J.R. and Aramayo,R.
Direct Submision
JOURNAL
Submitted (03-DEC-2002) Biology, Texas A&M University, BSW 415,
College Station, TX 77843-3258, USA
LOCATION/Qualifiers
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ACCESSION	AY189827.1	GI:28435537						
VERSION								
KEYWORDS								
SOURCE								
ORGANISM	his-3 integration vector pJHAM002							
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AUTHORS	other sequences; artificial sequences; vectors.							
TITLE	1 (bases 1 to 11373)							
JOURNAL	Lee,D.W., Haag,J.R. and Aramayo,R.							
	Construction of strains for rapid homokaryon purification after							
	integration of constructs at the hmc1dine-3 (his-3) locus of							
	Neurospora crassa							
	Curr. Genet. 43 (1), 17-23 (2003)							
PUBMED	12684841							
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AUTHORS	Lee,D.W., Haag,J.R. and Aramayo,R.							
TITLE	Direct Submission							
JOURNAL	Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,							
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 his-3 integration vector pJHAM004
 his-3 integration vector pJHAM004
 other sequences; artificial sequences; vectors.
 REFERENCE
 AUTHORS Lee,D.W., Haag,J.R. and Aramayo,R.
 TITLE Construction of strains for rapid homokaryon purification after integration of constructs at the histidine-3 (his-3) locus of Neurospora crassa
 JOURNAL Curr. Genet. 43 (1), 17-23 (2003)
 PUBMED 12684841
 REFERENCE 2 (bases 1 to 11403)
 AUTHORS Lee,D.W., Haag,J.R. and Aramayo,R.
 TITLE Direct Submision
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AUTHORS Kirchner, O. and Tauch, A.
TITLE Tools for genetic engineering in the amino acid-producing bacterium
JOURNAL Corynebacterium glutamicum
PUBMED J. Biotechnol. 104 (1-3), 287-299 (2003)
REFERENCE 2 (bases 1 to 3036)
AUTHORS Kirchner, O. and Tauch, A.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2003) Department of Genetics, University of
Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany

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Tools for genetic engineering in the amino acid-producing bacterium
Corynebacterium glutamicum
J. Biotechnol. 104 (1-3), 287-299 (2003)
12948646
2 (bases 1 to 3210)
Kirchner,O. and Rauch,A.
Submitted (15-JAN-2003) Department of Genetics, University of
Bielefeld, Universitaetstrasse 25, Bielefeld D-33615, Germany
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AUTHORS	Kirchner,O. and Tauch,A.
TITLE	Tools for genetic engineering in the amino acid-producing bacterium <i>Corynebacterium glutamicum</i>
JOURNAL	<i>J. Biotechnol.</i> 104 (1-3), 287-299 (2003)
PUBMED	12948646
REFERENCE	2 (bases 1 to 5869)
AUTHORS	Kirchner,O. and Tauch,A.
TITLE	Direct Submission
JOURNAL	Submitted (15-JAN-2003) Department of Genetics, University of
	Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
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VERSION AF445080.1 GI:17386067
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ORGANISM Cloning vector pEC-K18mob2
REFERENCE Cloning sequences; artificial sequences; vectors.
AUTHORS 1 (bases 1 to 5695)
Tauch,A., Kirchner,O., Löffler,B., Gotker,S., Puhler,A. and
Kalinowski,J.
TITLE Efficient Electroporation of Corynebacterium diphtheriae with
a Mini-Replicon Derived from the Corynebacterium glutamicum Plasmid
pGAI
JOURNAL Curr. Microbiol. 45 (5), 362-367 (2002)
PUBMED 12232668
REFERENCE 2 (bases 1 to 5695)
AUTHORS Tauch,A.
JOURNAL Direct Submission
TITLE Submitted (08-NOV-2001) Department of Genetics, University of
Bielefeld, Universitaetstrasse 25, Bielefeld D-33615, Germany
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2006, 16:47:46 ; Search time 1925 Seconds
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Title: US-09-921-143-36

Perfect score: 5283

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1

ABK10062 ID ABK10062 standard; DNA; 5283 BP.

XX ABK10062;

DT 21-MAY-2002 (first entry)

DE Expression vector construct pVGI.1 containing VEGF-2 insert.

XX Human; vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1;
XX chronic limb ischaemia; myocardial ischemia; autoimmune disorder; pHR4;
XX allergic reaction; organ rejection; inflammatory condition; arrhythmia;
XX hyperproliferative disorder; viral infection; bacterial infection;
XX fungal infection; parasitic infection; cardiovascular disorder; embolism;
XX heart valve disease; aneurysm; arterial occlusive disorder; gene therapy.

OS Synthetic.

PN WO200211769-A1.

PD 14-FEB-2002.

PF 03-AUG-2001; 2001WO-US024658.

PR 04-AUG-2000; 2000US-0223276P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Coleman TA;

PT WPI; 2002-217153/27.

XX Isolated nucleic acid having expression vector construct with vascular
XX endothelial growth factor-2 insert, useful for treating chronic limb
XX ischemia or myocardial ischemia, autoimmune disorders and allergic
XX conditions.

PS Disclosure; Fig 31; 241pp; English.

XX The invention relates to an isolated nucleic acid comprising pVGI.1
XX expression vector construct containing the vascular endothelial growth

CC factor 2 (VEGF-2) insert. The nucleic acid is useful for producing a host
 CC cell by transducing, transforming or transfecting a host cell with the
 CC DNA and for treating a patient having chronic limb ischaemia or
 CC myocardial ischaemia, or a disease or disorder selected from autoimmune
 CC disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or
 CC conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g.
 CC Crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease),
 CC diseases due to viral, bacterial, fungal or parasitic infection,
 CC cardiovascular disorders (e.g. cardiomyopathy), arrhythmia, heart valve
 CC disease, aneurysms, arterial occlusive disorders and embolism. This
 CC sequence represents the pVGI.1 expression vector containing the VEGF-2
 CC insert
 CC
 XX

SQ Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 U; 0 Other;

Query Match 100.0%; Score 5283; DB 6; Length 5283;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTGAACCTTATGAGCACTTCTTCTAGTACATCTACGATTAATGATCGCTAT 60
 DB 1 AAGCTTGAACCTTATGAGCACTTCTTCTAGTACATCTACGATTAATGATCGCTAT 60
 QY 61 TACCATGATGATGGGTTTGGCAGTACATCAATGGCGTGGATGGGTTGACTCAG 120
 DB 61 TACCATGATGATGGGTTTGGCAGTACATCAATGGCGTGGATGGGTTGACTCAG 120
 QY 121 GGGATTTCCAAAGTCTCCACCCCACTGACATGGAATGGAGTTTGTGGACCAAAATCA 180
 DB 121 GGGATTTCCAAAGTCTCCACCCCACTGACATGGAATGGAGTTTGTGGACCAAAATCA 180
 QY 181 ACGAGACTTTCCAAAGTGTGTACAACTCCGCCCATTTGACGCAATGGCGGTATAGGC 240
 DB 181 ACGAGACTTTCCAAAGTGTGTACAACTCCGCCCATTTGACGCAATGGCGGTATAGGC 240
 QY 241 AACATGCTTATGTAAACGGTGTAGCAACATGCTTATTAAGAGAGAAAAAGCAACCGTG 300
 DB 241 AACATGCTTATGTAAACGGTGTAGCAACATGCTTATTAAGAGAGAAAAAGCAACCGTG 300
 QY 301 CATGCCATTTGGTGGAGTAAAGGTGTATGATCGTGTATGATGTCCTTGTATGAGAG 360
 DB 301 CATGCCATTTGGTGGAGTAAAGGTGTATGATCGTGTATGATGTCCTTGTATGAGAG 360
 QY 361 GCAACAGACGGGTCTAACAGGATTTGACGAAACCACTGAATTCGCAATTGACAGATATT 420
 DB 361 GCAACAGACGGGTCTAACAGGATTTGACGAAACCACTGAATTCGCAATTGACAGATATT 420
 QY 421 GTATTTAAGTCCAGCTCGATACATTAACGCAATTGACCAATTTGATGATG 480
 DB 421 GTATTTAAGTCCAGCTCGATACATTAACGCAATTGACCAATTTGATGATG 480
 QY 481 CACCTGGGTTGGATTCATCATCATGCACTCGTGGGCTTCTCTGTGGGCTGTCTT 540
 DB 481 CACCTGGGTTGGATTCATCATCATGCACTCGTGGGCTTCTCTGTGGGCTGTCTT 540
 QY 541 CTGCTGCGCGTGGCTGCTCCGGGTCCTGCGAGAGGCGCCGCGCGCGCGCGCTTC 600
 DB 541 CTGCTGCGCGTGGCTGCTCCGGGTCCTGCGAGAGGCGCCGCGCGCGCGCGCTTC 600
 QY 601 GAGTCCGGAAGTCTGAGAGCGGAGGCGCGAGCGCGGTTGAGGCAAGGCTTATGCA 660
 DB 601 GAGTCCGGAAGTCTGAGAGCGGAGGCGCGAGCGCGGTTGAGGCAAGGCTTATGCA 660
 QY 661 AGCAAAAGTCTGAGAGGAGCAATTAAGTCTGTGTCTCAATGAACTCATACATGTA 720
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 DB 721 CTACCAAGAAATTTGAGAAATGTAACAAGTCTAGCTTAAGAAAGAGGCTGGCAACAT 780
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 DB 841 CATTATTAATACAGAGATCTTTGAAAAGTATGATGATGAGAGAAAGCTCAATGCATG 900
 QY 901 CCAAGGAGAGTGTATGATGATGAGAGAGGATTTGAGTGGCGCAAAACCTTCTT 960
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 DB 1861 TCTTTCTACACCAATGATGATCCCGCGGAGTGTGAGAGCCCAAGATTAAGCTGTGCTCCT 1920

QY 1921 GAATTCATCCCAAGTCTAACTACCTGTTTGTCTTCAACCCTTGAGACCTTGTAAATT 1980
DB 1921 GAATTCATCCCAAGTCTAACTACCTGTTTGTCTTCAACCCTTGAGACCTTGTAAATT 1980
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Qy 3066 GTAGCAAAAGGCGCAGCAAAAGGCGGAGAACCGTAAAGGCGGTTGCTGCGCTTTT 3125
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Db 6991 GAGATTAATCGTCAGCAAGCGGCACTGTCCTCCCACTCTGCAAGTTCGCGGCGATG 7024
Qy 3846 GATGCGCGGATAGCCGCTGCTGCTTCTGAGATGCCAGCGATTTGCACTGCCGTAGAA 3905

Db 7025 ----- 7024
Qy 3906 CTCGCGAGGTCGTCACAGCTCAAGCAGACAGTGAACCACTCCGAGAGGATCGAGCCC 3965
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Db 10222 ----- 10221
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Db 10644 TCCTCGCGGTGCGGCGCATGCGCGCTTGAAGCTTGCGCAACGATTGGCTGCGCGCAGCCCC 10703
QY 4446 TGATGCTCTTCGTCAGATCATCTGATTCGACAAAGCCGCTTCATCCGAGTACGTGCT 4505
Db 10704 TGATGCTCTTCGTCAGATCATCTGATTCGACAAAGCCGCTTCATCCGAGTACGTGCT 10763
QY 4506 CGCTCGATGCGATTTTTCCTGCTGGTGTCAATGGGAGGATGCGGATCAAGGTAATGC 4565
Db 10764 CGCTCGATGCGATTTTTCCTGCTGGTGTCAATGGGAGGATGCGGATCAAGGTAATGC 10823
QY 4566 AGCGCGCGCATTTGATGAGCATGATGATATCTTTCTCGGCAAGAGCAAGGTGATGATGAC 4625
Db 10824 AGCGCGCGCATTTGATGAGCATGATGATATCTTTCTCGGCAAGAGCAAGGTGATGATGAC 10883

QY 4626 AGGAGATCTTCGCCCCGCACTTCGCCCAATAGACAGCCAGTCCCTTCCGCTTCACTGACACA 4685
Db 10884 AGGAGATCTTCGCCCCGCACTTCGCCCAATAGACAGCCAGTCCCTTCCGCTTCACTGACACA 10943
QY 4686 ACGTGCAGCAGACTGCGGCAAGAAAGCGCGCTGTGCGCAGCCAGATAGCGCGCTGCC 4745
Db 10944 ACGTGCAGCAGACTGCGGCAAGAAAGCGCGCTGTGCGCAGCCAGATAGCGCGCTGCC 11003
QY 4746 TCGTCTCGCACTTCAATTCAGGGGCAACCGGACAGGTTCGCTTGAACAAAAGAACCGGGGCGC 4805
Db 11004 TCGTCTCGCACTTCAATTCAGGGGCAACCGGACAGGTTCGCTTGAACAAAAGAACCGGGGCGC 11063
QY 4806 CCTGCGCTGACAGCCCGGAAACAGCGCGCATCAAGCAGCGATTTGTTGTGCGCAG 4865
Db 11064 CCTGCGCTGACAGCCCGGAAACAGCGCGCATCAAGCAGCGATTTGTTGTGCGCAG 11123
QY 4866 TCATAGCCGAATAGCTCTTCACCCCAAGCGGCGGAGAACTGCGTGCATCATCTTGT 4925
Db 11124 TCATAGCCGAATAGCTCTTCACCCCAAGCGGCGGAGAACTGCGTGCATCATCTTGT 11183
QY 4926 TCATCATGCGGAAACGATTCCTCATCTCTGTCTTGTATCAATCTTGATCCCTGCGCAT 4985
Db 11184 TCATCATGCGGAAACGATTCCTCATCTCTGTCTTGTATCAATCTTGATCCCTGCGCAT 11243
QY 4986 CAGATCCTTGCGCGCAAGAAAGCCATCAGTTTACTTTCAGGAGCTTCCCAACCTTACCA 5045
Db 11244 CAGATCCTTGCGCGCAAGAAAGCCATCAGTTTACTTTCAGGAGCTTCCCAACCTTACCA 11303
QY 5046 GAGGGCGCCCCAGCTGCAATTCGATTCGCTTGTGCTGCTGCAATAAAACCGCCAGTCTAGC 5105
Db 11304 GAGGGCGCCCCAGCTGCAATTCGATTCGCTTGTGCTGCTGCAATAAAACCGCCAGTCTAGC 11363
QY 5106 TATGCGCATGTAAAGCCCACTGCAAGCTTACTGCTTCTCTTGGCGTTGGCTTTCCCTT 5165
Db 11364 TATGCGCATGTAAAGCCCACTGCAAGCTTACTGCTTCTCTTGGCGTTGGCTTTCCCTT 11423
QY 5166 GTCCAGATAGCCCGATGAGTGAATTCATTCGCGGGGTGAGACCGGTTCTGCGGAGTGGCT 5225
Db 11424 GTCCAGATAGCCCGATGAGTGAATTCATTCGCGGGGTGAGACCGGTTCTGCGGAGTGGCT 11483
QY 5226 TTCTACGTGTTCGCTTCTCTTTCAGACGCTTGGCGCCCTGAGTCTTTCGCGCAGCGTG 5283
Db 11484 TTCTACGTGTTCGCTTCTCTTTCAGACGCTTGGCGCCCTGAGTCTTTCGCGCAGCGTG 11541

RESULT 4
AAV29673/c
ID AAV29673 standard; cDNA; 6136 BP.
XX
AC AAV29673;
XX
DT 01-SEP-1998 (first entry)
XX
XX Hybrid NAMK.6 (termyl-1-linker-CBDEGV) nucleotide sequence.
DE
XX Search; liquefaction; sweetener; enzyme hybrid; endoglycanase; enzyme;
KW cellulose binding domain; CBD; starch processing; alpha-amylase;
KW saccharification; Termyl-1-linker-CBD fusion; ss.
XX
OS *Bacillus* sp.
XX *Humicola insolens*.
XX
PN M09816633-A1.
XX
PD 23-APR-1998.
XX
PF 13-OCT-1997; 97MO-DK000448.
XX
PR 11-OCT-1996; 96DK-00001130.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Bjornvad M, Pedersen S, Schuilein M, Biegaardfrantzen H;

XX WPI; 1998-251283/22.
 XX LIquefaction of starch for. e.g. production of sweeteners - comprises use
 PT of enzyme hybrids including cellulose binding domain for starch.
 XX
 PS Example 8; Page 65-67; 83pp; English.

XX This is the nucleotide sequence of the termamyl-linker-CBDEGV fusion
 CC construct pNBMK6.1. This is an enzyme hybrid which can be used for the
 CC liquefaction of starch. The enzyme hybrids contain amino acid sequences
 CC of alpha-amylase linked to a cellulose binding domain (CBD). The CBD is
 CC selected from the Bacillus or Cellulomonas endoglucanase, C. xylanase A
 CC or the Humicola insolens EGV sequence. The starch is liquefied by
 CC treating, in aqueous medium, with such an enzyme hybrid. A recombinant
 CC expression vector comprising a construct containing isolated DNA encoding
 CC enzyme hybrids with amylolytic activity, promoter and stop signals can be
 CC used to transform host cells for the production of the recombinant enzyme
 CC hybrids. The enzyme hybrids are useful in industrial starch processing
 CC especially for the production of sweeteners. Hybrid enzymes have altered
 CC affinity for substrate and increased activity, resulting in at least 1 of
 CC reduced calcium ion dependence, reduced formation of Maillard reaction
 CC products and reduced effect of alpha-amylase on subsequent
 CC saccharification

XX Sequence 6136 BP; 1475 A; 1545 C; 1712 G; 1404 T; 0 U; 0 Other;

Query Match 38.2%; Score 2017.2; DB 2; Length 6136;
 Best Local Similarity 91.8%; Pred. No. 5.7e-297;
 Matches 2203; Conservative 0; Mismatches 53; Indels 144; Gaps 1;

QY	2884	CAGCTGATTATGATATGCGCAACGCGGGGAGAGCGGTTGCGATATGGCGGCTCT	2943
DB	4381	CATATGCGGTGTGAATAACGACAGATCGTAAAGAAAATACCGCATCAGCGCTCT	4322
QY	2944	TCCGGTTCTGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3003
DB	4321	TCCGGTTCTGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4262
QY	3004	GCTCACTCAAAAGCGGTATATACGTTATCAAGATCAAGGAGATTAACGACGAAAGAAC	3063
DB	4261	GCTCACTCAAAAGCGGTATATACGTTATCAAGATCAAGGAGATTAACGACGAAAGAAC	4202
QY	3064	ATGTGAGCAAAAGCGGTATATACGTTATCAAGATCAAGGAGATTAACGACGAAAGAAC	3123
DB	4201	ATGTGAGCAAAAGCGGTATATACGTTATCAAGATCAAGGAGATTAACGACGAAAGAAC	4142
QY	3124	TTCCATAGGCTCCGCCCCCTGACGAGCATCAAAATTCAGCTCAAGTCAAGGTGG	3183
DB	4141	TTCCATAGGCTCCGCCCCCTGACGAGCATCAAAATTCAGCTCAAGTCAAGGTGG	4082
QY	3184	CGAAACCGGACGAGCTATTAAGATACAGGCGGTTCCCTCGGAAGCTCCCTGCTGGC	3243
DB	4081	CGAAACCGGACGAGCTATTAAGATACAGGCGGTTCCCTCGGAAGCTCCCTGCTGGC	4022
QY	3244	TCTCTGTTTCGACCTCGCGCTTACCGGATACCTGTCGCGCTTCTCTTCGCGAAGC	3303
DB	4021	TCTCTGTTTCGACCTCGCGCTTACCGGATACCTGTCGCGCTTCTCTTCGCGAAGC	3962
QY	3304	GTGGGCTTTTCTCATAGCTCAAGCTGTAGATCTCAAGTTCGCTGAGTGGTCTGCTCC	3363
DB	3961	GTGGGCTTTTCTCATAGCTCAAGCTGTAGATCTCAAGTTCGCTGAGTGGTCTGCTCC	3902
QY	3364	AAAGCTGGGTGTGTGACGAACCCCGCTTACGCGCCGACCGCTGCGCTTATCCGCTAAC	3423
DB	3901	AAAGCTGGGTGTGTGACGAACCCCGCTTACGCGCCGACCGCTGCGCTTATCCGCTAAC	3842
QY	3424	TATCGCTTGAATCAACCGGTATAGACAGACTTATCGCTGACGACGACCTGCTGCT	3483
DB	3841	TATCGCTTGAATCAACCGGTATAGACAGACTTATCGCTGACGACGACCTGCTGCT	3782
QY	3484	AAAGGATTAGACGAGCGGTATAGCGGTGCTACAGAGTTCTTGAAATGCTGGCT	3543

DB	3781	AAAGGATTAGACGAGCGGTATAGCGGTGCTACAGAGTTCTTGAAATGCTGGCT	3722
QY	3544	AACTACGCTACACTAGAAAGAAAGATATTTGGTATCTGCGCTTCTGCTTAACCGATTACC	3603
DB	3721	AACTACGCTACACTAGAAAGAAAGATATTTGGTATCTGCGCTTCTGCTTAACCGATTACC	3662
QY	3604	TTTCGAAAAAGATTGTAGCTCTGATCCGCAAAACCAACACCGCTGTAGCGGTGT	3663
DB	3661	TTTCGAAAAAGATTGTAGCTCTGATCCGCAAAACCAACACCGCTGTAGCGGTGT	3602
QY	3664	TTTTTGTGTTCAGACAGAGATTAACGCGAGAAAAAGATCTCAAGAAATCTTTTG	3723
DB	3601	TTTTTGTGTTCAGACAGAGATTAACGCGAGAAAAAGATCTCAAGAAATCTTTTG	3542
QY	3724	ATCTTTTTCAGCGGCTTGAAGCTCAAGGAAACGAAATCTCAAGGATTTGGTC	3783
DB	3541	ATCTTTTTCAGCGGCTTGAAGCTCAAGGAAACGAAATCTCAAGGATTTGGTC	3482
QY	3784	ATGAGATTATCGTCGACCAACGCGCCATCTGCTCCCACTCTGCAATTCGCGGCA	3843
DB	3481	ATGAGATTATCAAAAAGATCTTCACTAGATCTT-----	3446
QY	3844	TGAGTGCAGGATAGCCGCTGCTGTTCTTGATGCCGACGAGATTTCATCCCGGTAG	3903
DB	3445	-----	3446
QY	3904	AACTCCGCGAGGTCTGTCAGCCTCAGCGACGAGCTGAACCAACTCGCGAGGGATCGAGC	3963
DB	3445	-----	3446
QY	3964	CCGGGGTGGCGAAGAACTCAGCATGAGATCCCGCTGAGAGATCATCCGCGCG	4023
DB	3445	TGGGGTGGCGAAGAACTCAGCATGAGATCCCGCTGAGAGATCATCCGCGCG	3386
QY	4024	TCCCGAAAAAGATTCGGAAGCCCACTTTATGAAGAGCGCGGTGAATCAAGATCT	4083
DB	3385	TCCCGAAAAAGATTCGGAAGCCCACTTTATGAAGAGCGCGGTGAATCAAGATCT	3326
QY	4084	CGTATGCGAGGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	4143
DB	3325	CGTATGCGAGGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3266
QY	4144	AGAACTGTCAGAAAGCGATAGAGAGCGATGCTGCGAATCGGAGCGCGATTCGCT	4203
DB	3265	AGAACTGTCAGAAAGCGATAGAGAGCGATGCTGCGAATCGGAGCGCGATTCGCT	3206
QY	4204	AAAGCAAGAGAGCGGTGAGCCCATTCGCGCAAGCTCTTCAGCAATATCAAGGCTAG	4263
DB	3205	AAAGCAAGAGAGCGGTGAGCCCATTCGCGCAAGCTCTTCAGCAATATCAAGGCTAG	3146
QY	4264	CCAAGCTATGCTCTATAGCGGTCCGCAACCCAGCGCGCAAGTGGATTCAG	4323
DB	3145	CCAAGCTATGCTCTATAGCGGTCCGCAACCCAGCGCGCAAGTGGATTCAG	3086
QY	4324	AAAAAGCGCAATTTTCCACATATATTTGGCAAGAGATTCGATGGGTTCACAGCA	4383
DB	3085	AAAAAGCGCAATTTTCCACATATATTTGGCAAGAGATTCGATGGGTTCACAGCA	3026
QY	4384	GATTCCTGCGGTGGGAGATGCGCGCTTGAAGCTTGGCGAACAATTCGCGTGGCGAGCC	4443
DB	3025	GATTCCTGCGGTGGGAGATGCGCGCTTGAAGCTTGGCGAACAATTCGCGTGGCGAGCC	2966
QY	4444	CTGATGCTCTTCTGTCAGATCAATCTGATCGAACAGCGGCTTCATCCGATACGTG	4503
DB	2965	CTGATGCTCTTCTGTCAGATCAATCTGATCGAACAGCGGCTTCATCCGATACGTG	2906
QY	4504	CTGCTGATGCGATGTTTTCGCTTGTGTGCGAATGGCGAGTACCGGATCAAGGGTAT	4563
DB	2905	CTGCTGATGCGATGTTTTCGCTTGTGTGCGAATGGCGAGTACCGGATCAAGGGTAT	2846
QY	4564	GAGCGCGCGCATGTCATCAAGCATGATGATCTTTCTCGGAGAGCAAGGTGAGATG	4623
DB	2845	GAGCGCGCGCATGTCATCAAGCATGATGATCTTTCTCGGAGAGCAAGGTGAGATG	2786

QY 4624 ACAGAGATCTGCCCCGCACTTGGCCCAATAGCAGCAGTCCCTTCCCGTTGANGA 4683
XX
DB 2785 ACAGAGATCTGCCCCGCACTTGGCCCAATAGCAGCAGTCCCTTCCCGTTGANGA 2726
XX
QY 4684 CAACTGCAAGCAGCTGCGCAAGAAAGCCGCTGTGCGCAAGCAATAGCCGCGTG 4743
XX
DB 2725 CAACTGCAAGCAGCTGCGCAAGAAAGCCGCTGTGCGCAAGCAATAGCCGCGTG 2666
XX
QY 4744 CCTGCTCTGCAAGTTCATTGAGGGACCGGACAGGTGCGGTCTTGAACAAAAGACCGGCG 4803
XX
DB 2665 CCTGCTCTGCAAGTTCATTGAGGGACCGGACAGGTGCGGTCTTGAACAAAAGACCGGCG 2606
XX
QY 4804 GCCCTGCGCTGACAGCCGCAACAGCGGCGCATCAGACAGCCGATTTGTCTTGTGCGC 4863
XX
DB 2605 GCCCTGCGCTGACAGCCGCAACAGCGGCGCATCAGACAGCCGATTTGTCTTGTGCGC 2546
XX
QY 4864 AGTCATAGCCGAATAGCTCTTCCACCAAGCGCGCGAAGAACTGCGCAATCATCTT 4923
XX
DB 2545 AGTCATAGCCGAATAGCTCTTCCACCAAGCGCGCGAAGAACTGCGCAATCATCTT 2486
XX
QY 4924 GTTCAATATGCGAAAGCATCTCTATCTGCTCTTATTCAGATCTTGAATCCCTGCGCC 4983
XX
DB 2485 GTTCAATATGCGAAAGCATCTCTATCTGCTCTTATTCAGATCTTGAATCCCTGCGCC 2426
XX
QY 4984 ATCAGATCTTGGCGGCAAGAAAGCATCAGATTACTTTGAGGGCTTCCCAACTTAC 5043
XX
DB 2425 ATCAGATCTTGGCGGCAAGAAAGCATCAGATTACTTTGAGGGCTTCCCAACTTAC 2366
XX
QY 5044 CAGAGGCGCGCCAGCTGCGCAATTCGGTTGCTGTGTCATTAACCGCCCAAGTCTA 5103
XX
DB 2365 CAGAGGCGCGCCAGCTGCGCAATTCGGTTGCTGTGTCATTAACCGCCCAAGTCTA 2306
XX
QY 5104 GCTATCGCATGTAAAGCCCAATGCAAGTACTCTTCTCTTGGCGTTTCCGTTTCC 5163
XX
DB 2305 GCTATCGCATGTAAAGCCCAATGCAAGTACTCTTCTCTTGGCGTTTCCGTTTCC 2246
XX
QY 5164 TTGTCCAGATAGCCCAATGCAAGTACTCTTCTCTTGGCGTTTCCGTTTCC 5223
XX
DB 2245 TTGTCCAGATAGCCCAATGCAAGTACTCTTCTCTTGGCGTTTCCGTTTCC 2186
XX
QY 5224 CTTTCTAGTGTTCGCTTCTTGTAGCAGCCCTTGCCTGAGTGTCTTGGCGAGCGTG 5283
XX
DB 2185 CTTTCTAGTGTTCGCTTCTTGTAGCAGCCCTTGCCTGAGTGTCTTGGCGAGCGTG 2126
XX

RESULT 5
AAK52020/c
ID AAK52020 standard; DNA; 4800 BP.
XX

AAK52020;
AC
XX
DT 18-JUN-1999 (first entry)
XX
DE Synthetic DNA plasmid sequence synlux4.
XX
KM DNA plasmid; lux A; lux B; Vibrio fischeri; luciferase; promoter;
XX
KM ttn9 kanamycin/neomycin phosphotransferase; DNA synthesis;
XX
KM replication competent double-stranded polynucleotide; ss.
XX
OS Synthetic.
XX
PN WO9914318-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-US019312.
XX
PR 16-SEP-1997; 97US-0059017P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Evans GA;

XX
DR WPI; 1999-244029/20.
XX
PT Synthesis of replication competent double-stranded polynucleotides.
XX
PS Example 4; Fig 4A-C; 135pp; English.
XX
CC The present sequence represents a synthetic DNA plasmid sequence,
CC designed using synthetic parts of known plasmids. Within the sequence
CC included the sequences of lux A, lux B, the A and B components of the
CC Vibrio fischeri luciferase sequence, positions of pUC19 including the
CC origin of replication and replication stability sequences, and the
CC promoter and coding sequence for ttn9 kanamycin/neomycin
CC phosphotransferase. The plasmid was synthesised from 192 50-mers (see
CC AAK52021-12) to demonstrate the method of the invention. The
CC specification describes a method for the synthesis of replication
CC competent double-stranded polynucleotides. The method comprises
CC generating a first set of oligonucleotides corresponding to the plus
CC strand and a second set corresponding to the minus strand and annealing.
CC The method can be used for preparing polynucleotides encoding sequences
CC involved in a biochemical pathway. In particular, they can be used to
CC produce polynucleotides encoding enzymes, e.g. hexokinase, phosphohexose
CC isomerase, phosphofructokinase-1, aldolase, triose-phosphate isomerase,
CC glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate kinase,
CC phosphoglycerate mutase, enolase or pyruvate kinase. They can also be
CC used for the preparation of viral particles, artificial genomes and
CC artificial genetic systems
XX
SQ Sequence 4800 BP; 1345 A; 1032 C; 1163 G; 1260 T; 0 U; 0 Other;

Query Match 33.9%; Score 1793.4; DB 2; Length 4800;
Best Local Similarity 91.8%; Pred. No. 49e-263;
Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1;

QY 3127 CATAGGCTCCGCCCCCTGAGAGCATCACAAAATGACGCTTACAGAGTGGCGA 3186
DB 4800 CATAGGCTCCGCCCCCTGAGAGCATCACAAAATGACGCTTACAGAGTGGCGA 4741
QY 3187 AACCCGACAGACATTAAGATACAGGCGTTTCCCTGGAAGTCCCTGCTGCTCT 3246
DB 4740 AACCCGACAGACATTAAGATACAGGCGTTTCCCTGGAAGTCCCTGCTGCTCT 4681
QY 3247 CCGTTCGCAACCCGCGCTTACCGGATACCTGCGCCTTTCCTCCCTGGGAAAGCGTG 3306
DB 4680 CCGTTCGCAACCCGCGCTTACCGGATACCTGCGCCTTTCCTCCCTGGGAAAGCGTG 4621
QY 3307 GCGCTTCTCATAGCTACGCTGATGATCTCAGTTGCGGTAGTGTGCTTCCCAAG 3366
DB 4620 GCGCTTCTCATAGCTACGCTGATGATCTCAGTTGCGGTAGTGTGCTTCCCAAG 4561
QY 3367 CTGGGCTGTGTGCAAGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGTTACTAT 3426
DB 4560 CTGGGCTGTGTGCAAGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGTTACTAT 4501
QY 3427 CGTCTTAGTCCAAACCGGTAAAGACAGACTTATTCGACATCGGAGAGGACACGTGTAAC 3486
DB 4500 CGTCTTAGTCCAAACCGGTAAAGACAGACTTATTCGACATCGGAGAGGACACGTGTAAC 4441
QY 3487 AGGATTAGCAGAGGAGTATGTAGCGGTGCTTACAGAGTCTTGAAGTGTGCGCTTAAC 3546
DB 4440 AGGATTAGCAGAGGAGTATGTAGCGGTGCTTACAGAGTCTTGAAGTGTGCGCTTAAC 4381
QY 3547 TAGGCTTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACTTC 3606
DB 4380 TAGGCTTACACTAGAAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACTTC 4321
QY 3607 GGAAGAAAGATTGTAGCTCTTGTATCGGCAAAACAAACGCGCTGTAGCGGTTGTTT 3666
DB 4320 GGAAGAAAGATTGTAGCTCTTGTATCCGCAAAACAAACGCGCTGTAGCGGTTGTTT 4261
QY 3667 TTTGTTTGAAGCAGAGATTACGCGCAGAAAAAAGATCTCAGAGAGATCTTTGATC 3726
DB 4260 TTTGTTTGAAGCAGAGATTACGCGCAGAAAAAAGATCTCAGAGAGATCTTTGATC 4201

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QY 3727 TTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCAGCTTAAGGAAATTTTGTCANG 3786
Db 4200 TTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCAGCTTAAGGAAATTTTGTCANG 4142
QY 3787 AGATTATCGTCGACCAAGGCGGCATCGTCTCCCACTCTGAGTTGGGGGCGATGG 3846
Db 4141 ----- 4142
QY 3847 ATGCGCGGATAGCCGCTGCTGTTTCTGTGATGCCAGCGATTGCACTGCGGTAGAAC 3906
Db 4141 ----- 4142
QY 3907 TCCGCGAGTTCGTCCAGCTCAGGCGACGACTGAACCACTCCGCGAGGGGATCGAGCCG 3966
Db 4141 -----GCCCC 4137
QY 3967 GGGTGGGCGGAAGAACTCCAGCATGAGATCCCGCGCTGAGAGTCAATCCAGCCGGGCTCC 4026
Db 4136 GGGTGGGCGGAAGAACTCCAGCATGAGATCCCGCGCTGAGAGTCAATCCAGCCGGGCTCC 4077
QY 4027 CGGAAAAAGATTCCGAAGCCCAACTTTCATAGAAAGCGGCGGTGAATGAATCTCGT 4086
Db 4076 CGGAAAAAGATTCCGAAGCCCAACTTTCATAGAAAGCGGCGGTGAATGAATCTCGT 4017
QY 4087 GATGCGAGTGGGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4146
Db 4016 GATGCGAGTGGGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3957
QY 4147 ACTGCTCAAGAAAGCGCATAGAAAGCGATGCGTGCATGCGGAGCGGCGATCCGTA 4206
Db 3956 ACTGCTCAAGAAAGCGCATAGAAAGCGATGCGTGCATGCGGAGCGGCGATCCGTA 3897
QY 4207 GCAAGAAAGCGATGAGCCCATTCGCGCAAGCTTCTTCAAGATATCAAGGATAGCA 4266
Db 3896 GCAAGAAAGCGATGAGCCCATTCGCGCAAGCTTCTTCAAGATATCAAGGATAGCA 3837
QY 4267 AGCCTATGCTCTATAGCGGCTCCGCCACACCGCGCGCAAGTGCATGATATCCAGAAA 4326
Db 3836 AGCCTATGCTCTATAGCGGCTCCGCCACACCGCGCGCAAGTGCATGATATCCAGAAA 3777
QY 4327 AGGCGCATTTTCCACCATGATATTCGGCAAGAGGATGCGATGGGTACAGACGAGAT 4386
Db 3776 AGGCGCATTTTCCACCATGATATTCGGCAAGAGGATGCGATGGGTACAGACGAGAT 3717
QY 4387 CTTGCGCGTGGGCAATGCGCGCTTGAAGCTGCGGAAAGATTGCGTGGCGCGAGCCCT 4446
Db 3716 CTTGCGCGTGGGCAATGCGCGCTTGAAGCTGCGGAAAGATTGCGTGGCGCGAGCCCT 3657
QY 4447 GATGCTCTTGTGCAAGTCAATCTGATGCAAGACCGGCTTCATCCGAGTACGTGCTC 4506
Db 3656 GATGCTCTTGTGCAAGTCAATCTGATGCAAGACCGGCTTCATCCGAGTACGTGCTC 3597
QY 4507 GCTCGATGCGATGTTTCTTGGTGTGATGAGTGGGAGTAGGCGGATCAAGGATAGCA 4566
Db 3596 GCTCGATGCGATGTTTCTTGGTGTGATGAGTGGGAGTAGGCGGATCAAGGATAGCA 3537
QY 4567 GCGCGCGCATTTGATGAGCATGATGATGATCTTCTCGGAGAGACAGGTGATGATGACA 4626
Db 3536 GCGCGCGCATTTGATGAGCATGATGATGATCTTCTCGGAGAGACAGGTGATGATGACA 3477
QY 4627 GAGATGCTGCGCGCGGCACTTCCCAATAGACGACGATCCCTTCCCGCTTCAGTACAA 4686
Db 3476 GAGATGCTGCGCGCGGCACTTCCCAATAGACGACGATCCCTTCCCGCTTCAGTACAA 3417
QY 4687 CGTCCGACAGCTGCGCAAGAAAGCGCGCTGCTGCGCAAGTATGAGCGCGCTGCT 4746
Db 3416 CGTCCGACAGCTGCGCAAGAAAGCGCGCTGCTGCGCAAGTATGAGCGCGCTGCT 3357
QY 4747 CGTCCGACAGTTCATTCAGGGCAACCGGACAGGTGCTTTCAGCAAAAAGACCGGGGCC 4806
Db 3356 CGTCCGACAGTTCATTCAGGGCAACCGGACAGGTGCTTTCAGCAAAAAGACCGGGGCC 3297
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QY 4807 CCTGGCTGACAGCCGGAAACAGGGGCGCATCAGACAGCCGATGCTGTGCGCCAGT 4866
Db 3296 CCTGGCTGACAGCCGGAAACAGGGGCGCATCAGACAGCCGATGCTGTGTGGCCAGT 3237
QY 4867 CATAGCCGATAGCTCTTCCACCCAAAGCGGCGGAGAACTGCGTGCATCTGTT 4926
Db 3236 CATAGCCGATAGCTCTTCCACCCAAAGCGGCGGAGAACTGCGTGCATCTGTT 3177
QY 4927 CAATCAGCGAAACGATCTCATCTGCTCTTGAATCAGATCTTGATCCCTGCGGCATC 4986
Db 3176 CAATCAGCGAAACGATCTCATCTGCTCTTGAATCAGATCTTGATCCCTGCGGCATC 3117
QY 4987 AGATCCTGGGGCGCAAGAAAGCATCCAGTTTACTTTGACAGGCTTCCCACTTAACGAG 5046
Db 3116 AGATCCTGGGGCGCAAGAAAGCATCCAGTTTACTTTGACAGGCTTCCCACTTAACGAG 3057
QY 5047 AGGGCGCCCACTGCGCAATTCGCGTTCGCTGCTGCTCATAAACCGCCAGTACGCT 5106
Db 3056 AGGGCGCCCACTGCGCAATTCGCGTTCGCTGCTGCTCATAAACCGCCAGTACGCT 2997
QY 5107 ATGCGCATGTAAGCCCACTGCAAGCTACTGCTTTCTCTTGGCGCTTTCCTTTG 5166
Db 2996 ATGCGCATGTAAGCCCACTGCAAGCTACTGCTTTCTCTTGGCGCTTTCCTTTG 2937
QY 5167 TCCAGTACCCAGTACGATGATTCATTCAGCGGGGTACAGACCGTTTCTGCGAGTGGCTT 5226
Db 2936 TCCAGTACCCAGTACGATGATTCATTCAGCGGGGTACAGACCGTTTCTGCGAGTGGCTT 2877
QY 5227 TCTACGTTTCCGCTTCTTTAGCAGCCCTTGCCTGAGTGTTCGGGACGCTG 5283
Db 2876 TCTACGTTTCCGCTTCTTTAGCAGCCCTTGCCTGAGTGTTCGGGACGCTG 2820

RESULT 6
ADT55139
ID ADT55139 standard; DNA; 4058 BP.
XX
AC ADT55139;
XX
DT 30-DEC-2004 (first entry)
XX
XX Nucleotide sequence of expression vector pMB1-hpRNAIpha.
XX
KW Ophthalmological; radiation; free radical; superoxide anion;
KW heavy metal cation; metallochionein; superoxide dismutase; SOD; catalase;
KW glutathione peroxidase 4; GPX-4; gamma glutamyl transpeptidase;
KW xeroderma; xeroderma; autoimmune disorder; Sjogren's syndrome;
KW graft-versus-host disease; systemic lupus erythematosus;
KW rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
KW psychogenic disorder; trauma; hepatitis C; cancer; mastectomy; ss.
XX
OS Homo sapiens.
OS Simian virus 40.
OS Synthetic.
FH
FH Key location/Qualifiers
FH intron 332..497
FT /tag= a
FT /note= "human beta-globin intron"
FT 347..503
FT /tag= b
FT /note= "SV40 late gene polyadenylation signal"
FT 471..1162
FT /tag= c
FT /note= "CMV promoter"
FT 551..1077
FT /tag= d
FT /note= "human interferon (IFN) alpha cDNA"
FT 1158..1825
FT /tag= e
FT /note= "ColEI ori from pBluescript SK+"
FT 1226..2020
FT /tag= f
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FT /gene= "kanamycin resistance gene"
 XX WO2004087873-A2.
 XX 14-OCT-2004.
 XX 26-MAR-2004; 2004WO-US009194.
 XX 26-MAR-2003; 2003US-0458793P.
 PR 25-MAR-2004; 2004US-0778889.
 XX (GENT-) GENTERIC INC.
 PA Bennett NJ, Chen Y;
 XX WPI, 2004-737685/72.
 DR
 XX
 PT Attenuating increases in concentrations of radiation-induced free
 PT radicals in a mammalian cell, comprises contacting the cell with one or
 PT more nucleic acids encoding proteins that neutralizes or eliminates a
 PT portion of free radicals.
 XX
 XX Claim 34; SEQ ID NO 5; 58bp; English.
 PS
 CC The specification describes a method for attenuating increases in
 CC concentrations of radiation-induced free radicals, superoxide anions or
 CC heavy metal cations in a mammalian cell. The method comprises contacting
 CC the cell with one or more nucleic acids encoding one or more proteins
 CC that are expressed in the cell and that neutralizes or eliminates a
 CC portion of the free radicals, superoxide anions or heavy metal cations in
 CC the cell. The proteins are selected from metallothionein, superoxide
 CC dimutase, catalase, glutathione peroxidase (GPx)-4, or gamma-glutamyl
 CC transpeptidase. The method is useful for attenuating increases in
 CC concentrations of radiation-induced free radicals, superoxide anions or
 CC heavy metal cations in a mammalian cell, and ameliorating symptoms of
 CC xeroderma or xerophthalmia associated with conditions such as autoimmune
 CC disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus
 CC erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic
 CC dysfunction, conditions affecting the CNS, psychogenic disorder, trauma,
 CC hepatitis C, cancer and decrease in mastication. The present sequence
 CC represents an expression vector used in the method of the invention to
 CC express the relevant proteins.
 CC
 XX
 XX Sequence 4058 BP; 999 A; 1038 C; 1051 G; 970 T; 0 U; 0 Other;
 SQ
 Query Match 32.1%; Score 1697.8; DB 13; Length 4058;
 Best Local Similarity 86.7%; Pred. No. 1.6e-248;
 Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;
 QY 2706 CTAGAGCTAATCATGATGATAGCTGTTCCCTGTTGTAATTTGTAATCCGCTCAAAATTC 2765
 DB 1977 CTGGGCTTAATCATGATGATAGCTGTTCCCTGTTGTAATTTGTAATCCGCTCAAAATTC 2036
 QY 2766 ACACAAATATGAGCCGGAAGCATAAAGTAAAGCTGGGGTCTTAATGAGTACTA 2825
 DB 2037 ACACAAATATGAGCCGGAAGCATAAAGTAAAGCTGGGGTCTTAATGAGTACTA 2096
 QY 2826 ACTCACTTAATTCGTTGCGCTCACTGCCGCTTTTCAAGTCGGAAACCTGTGTTCC 2885
 DB 2097 ACTCACTTAATTCGTTGCGCTCACTGCCGCTTTTCAAGTCGGAAACCTGTGTTCC 2156
 QY 2886 GGTGCAATTAATGATGCGGCAACGCGGGGAGAGGGGTTTGGTATTTGGGCGCTTTC 2945
 DB 2157 GGTGCAATTAATGATGCGGCAACGCGGGGAGAGGGGTTTGGTATTTGGGCGCTTTC 2216
 QY 2946 CGCTTCTCTCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 3005
 DB 2217 CGCTTCTCTCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 2276
 QY 3006 TCACTCAAAAGCGGTAATGAGTATTCACAGAAATCAGGAGATACGAGGAAAGAAAT 3065
 DB 2277 TCACTCAAAAGCGGTAATGAGTATTCACAGAAATCAGGAGATACGAGGAAAGAAAT 2336

QY 3066 GTGACAAAAGGCGACGAAAAGGCGGTAATTAATTAATTAATTAATTAATTAATTAATTA 3125
 DB 2337 GTGACAAAAGGCGACGAAAAGGCGGTAATTAATTAATTAATTAATTAATTAATTAATTA 2396
 QY 3126 CCATAGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3185
 DB 2297 CCATAGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2456
 QY 3186 AAACCCGACGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3245
 DB 2457 AAACCCGACGAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2516
 QY 3246 TCCGTTCGACCGCTGCGGCTTACCGGATACCTGCTCCGCTTCCCTTCCGGAAGCGT 3305
 DB 2517 TCCGTTCGACCGCTGCGGCTTACCGGATACCTGCTCCGCTTCCCTTCCGGAAGCGT 2576
 QY 3306 GCGGCTTCTCATAGTCAAGCTGATAGTATCTCAAGTTCGATGATGATGATGATGATGAT 3365
 DB 2577 GCGGCTTCTCATAGTCAAGCTGATAGTATCTCAAGTTCGATGATGATGATGATGATGAT 2636
 QY 3366 GCTGGGCTGTGTGACGACACCCCGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3425
 DB 2637 GCTGGGCTGTGTGACGACACCCCGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2696
 QY 3426 TCGCTTGAAGTCCAAACCGGTAAGACAGACTTATGCGCACTGGCAGACGCACTGGTAA 3485
 DB 2697 TCGCTTGAAGTCCAAACCGGTAAGACAGACTTATGCGCACTGGCAGACGCACTGGTAA 2756
 QY 3486 CAGATTAGACAGAGCGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 3545
 DB 2757 CAGATTAGACAGAGCGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2816
 QY 3546 CTACGCTACACTAGAAAGACAGTATTTGATGATGATGATGATGATGATGATGATGATGAT 3605
 DB 2817 CTACGCTACACTAGAAAGACAGTATTTGATGATGATGATGATGATGATGATGATGATGAT 2876
 QY 3606 CGGAAAAGGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3665
 DB 2877 CGGAAAAGGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2936
 QY 3666 TTTTGTTCGACAGACAGATTAACGCGCAGAAAAGGATGATCAAGAAATCTTTGAT 3725
 DB 2937 TTTTGTTCGACAGACAGATTAACGCGCAGAAAAGGATGATCAAGAAATCTTTGAT 2996
 QY 3726 CTTTTCGACAGAGTCTGACGCTGATGAAAGAAAATCACTGATTAAGATTTTGTGAT 3785
 DB 2997 CTTTTCGACAGAGTCTGACGCTGATGAAAGAAAATCACTGATTAAGATTTTGTGAT 3056
 QY 3786 GAGATTATGTCGACCAAGGCGCATCGCTCCCACTCCTGCAATTCCGGGGGATG 3845
 DB 3057 GAG- 3059
 QY 3846 GATGCGGATAGCCGCTGCTGTTCTGATGATGCGAGATTTGCACTGCGGTAGAA 3905
 DB 3060 3059
 QY 3906 CTCGCGAGGTCTGACGCTCAGGACAGCTGAACCACTGCGAGAGGATCGAGCCC 3965
 DB 3060 3100
 QY 3966 GGGGTGGGGAAGAACTCCAGCATGAGATCCCGCGCTGAGGATCATCCAGCGGCGTC 4025
 DB 3101 GGGGTGGGGAAGAACTCCAGCATGAGATCCCGCGCTGAGGATCATCCAGCGGCGTC 3160
 QY 4026 CCGGAAAAGATTCGAGAGCCCACTTTCAATGAAGGCGGCGGTGAATTCGAATCTCG 4085
 DB 3161 ATGCGTAAGGAAATATCCGATCAAGAAATTTGTAAGCTTAATAT- 3208
 QY 4086 TGATGCGAGTTGGGCGTCTGTTGTCATTTTGAACCCCAAGTCCCGCTCAGAG 4145
 DB 3209 3215
 QY 4146 AACTCGTCAAGAAAGGCGATGAAAGGCGATGCGCTGCGAATCGGAGCGGCGATACCGTTAA 4205

OY	3006	TCACGCAAAAGCGGTAATAACGGTTATCCAGAAATCAGGGGTAACGAGAAATAAAT	3065
Db	2406	TCACGCAAAAGCGGTAATAACGGTTATCCAGAAATCAGGGGTAACGAGAAATAAAT	2465
OY	3066	GTGACAAAAGCGCCAGCAAAAGGCGAGAACCGTAAAAAGGCGCGTTGCTGGCCTTTT	3125
Db	2466	GTGAGCAAAAAGCGCCAGCAAAAGGCGAGAACCGTAAAAAGGCGCGTTGCTGGCCTTTT	2525
OY	3126	CCATAGGCTCCGCCCCCTCGACGACATCACAAAAATGACGCTCAATCAGAGTGGCG	3185
Db	2526	CCATAGGCTCCGCCCCCTCGACGACATCACAAAAATGACGCTCAATCAGAGTGGCG	2585
OY	3186	AAACCCGACAGGACTATATAAGATACAGAGCGTTTCCCTCGAAAGCTCCCTGTCGCTC	3245
Db	2586	AAACCCGACAGGACTATATAAGATACAGAGCGTTTCCCTCGAAAGCTCCCTGTCGCTC	2645
OY	3246	TCCTGTTCGACCCCTGCGCTTACCGGATACCTGTGCGGCTTTCTCCCTCGGAAAGCGT	3305
Db	2646	TCCTGTTCGACCCCTGCGCTTACCGGATACCTGTGCGGCTTTCTCCCTCGGAAAGCGT	2705
OY	3306	GGCGCTTCTCATAGCTACGCTGTAGGATATCTCAATTCCGTAAGCTGTTCCGTTCCAA	3365
Db	2706	GGCGCTTCTCATAGCTACGCTGTAGGATATCTCAATTCCGTAAGCTGTTCCGTTCCAA	2765
OY	3366	GCTGGGCTGTGTGACGAAACCCCGTTCAGGCCGACCGCTGCGCTTATCCGTAATCTA	3425
Db	2766	GCTGGGCTGTGTGACGAAACCCCGTTCAGGCCGACCGCTGCGCTTATCCGTAATCTA	2825
OY	3426	TCGCTCTTGAATGCCAACCCCGGTAAGACACAGACTTATCGCACTGGCAGACGCACTGTAA	3485
Db	2826	TCGCTCTTGAATGCCAACCCCGGTAAGACACAGACTTATCGCACTGGCAGACGCACTGTAA	2885
OY	3486	CAGATTATGACAGAGGAGTATGTATAGCGGTCTACAGAGTTCTTGAAGTGGTGCTTAA	3545
Db	2886	CAGATTATGACAGAGGAGTATGTATAGCGGTCTACAGAGTTCTTGAAGTGGTGCTTAA	2945
OY	3546	CTACGGCTACACTTAGAAGACAAGTATTTGGTATCTGCGCTCTGCTGAAGCAATTACCTT	3605
Db	2946	CTACGGCTACACTTAGAAGACAAGTATTTGGTATCTGCGCTCTGCTGAAGCAATTACCTT	3005
OY	3606	CGGAAAAAGATTGGTAGCTCTGATATCCGGGAAACAAACCCGTGTACCGGTGGTTT	3665
Db	3006	CGGAAAAAGATTGGTAGCTCTGATATCCGGGAAACAAACCCGTGTACCGGTGGTTT	3065
OY	3666	TTTTGTTTGCACGACGACAGATTACGCGCAGAAAAAAGATCTCAAGAAAGATCCTTGGAT	3725
Db	3066	TTTTGTTTGCACGACGACAGATTACGCGCAGAAAAAAGATCTCAAGAAAGATCCTTGGAT	3125
OY	3726	CTTTTTCATCGGGGTCTGACGCTCAAGTGAACGAAATCTCAGTTAAGGATTTTGGTCAT	3785
Db	3126	CTTTTTCATCGGGGTCTGACGCTCAAGTGAACGAAATCTCAGTTAAGGATTTTGGTCAT	3185
OY	3786	GAGATTATCGTCGACCAAAAGCGGACATGTCCTCCCACTTCGACAGTTGCGGGGCAATG	3845
Db	3186	GAG-----	3188
OY	3846	GATCGCGGATAGCCGCTGCTGTTTCTGTGATGCCAGCGAATTTCGACTCGCGGTAGAA	3905
Db	3189	-----	3188
OY	3906	CTCCGCGAGTCTGTCAGGCTCAGGACAGACCTGAACCACTCCGAGGGATGAGCGCC	3965
Db	3189	-----CGGATACATATTGTAATGTATTTAGAAAAATATACAAATAG	3229
OY	3966	GGGGTGGGCGAAGAACTTCAGACATGAGATCCCGCGCTGAGAGATCATCCAGCCGCGCTC	4025
Db	3230	GGGTTTCGCGCACTTTCGCCGAAAGGCGCACCTGTATGCGGTGTGAAATACCGCACAG	3289
OY	4026	CCGGAATAACGATTCGAAAGCCCAACTTTCACTAAGAGCGCGCGGTGTGAATCGAAATCTCG	4085
Db	3290	ATGCGTATAGGGAATAATCCGCATACAGAAATTGTAAAGCTTTAATAT-----	3337

QY	4066	TAATGACGAGTTGGGCGGTGGTGGTCATTTCCAAACCAGAGTCCCGCTCAGAAAG	4145
Db	3338	-----TCAAGA	3344
QY	4146	AACTGTCAGAAAGGCGATAGAAAGCGATGCGCTGCGAATTCGGAGCGCGCATCCGTA	4205
Db	3345	AACTGTCAGAAAGGCGATAGAAAGCGATGCGCTGCGAATTCGGAGCGCGCATCCGTA	3404
QY	4206	AGCAGAGAAAGCGGTCAAGCCCATTCGCGCGCAAGCTCTTCAGCAATATCAAGGGTAC	4265
Db	3405	AGCAGAGAAAGCGGTCAAGCCCATTCGCGCGCAAGCTCTTCAGCAATATCAAGGGTAC	3464
QY	4266	AACGCTATGTCCTGATAGCGGTCCGCCACACCGAGCGCGCAAGTCGATGAATCCGAA	4325
Db	3465	AACGCTATGTCCTGATAGCGGTCCGCCACACCGAGCGCGCAAGTCGATGAATCCGAA	3524
QY	4326	AAGCGGCATTTTCCACCATATATTTGCGCAAGAGGCGATTCGCCATGGGTCAAGACGA	4385
Db	3525	AAGCGGCATTTTCCACCATATATTTGCGCAAGAGGCGATTCGCCATGGGTCAAGACGA	3584
QY	4386	TCTTCGCGGTGCGGCATAGCGGCTTTGAGCCTTGCGAAGTTTCGCTGCGCGAGCCC	4445
Db	3585	TCTTCGCGGTGCGGCATAGCGGCTTTGAGCCTTGCGAAGTTTCGCTGCGCGAGCCC	3644
QY	4446	TGATGCTTTTGTCCAGATCATCTGATTCGACAAAGACCGGCTTCATTCGAGTACGTGCT	4505
Db	3645	TGATGCTTTTGTCCAGATCATCTGATTCGACAAAGACCGGCTTCATTCGAGTACGTGCT	3704
QY	4506	CGCTCGATGCGATGTTTCGCTTGGTGGTTCGATAGGGCAGGTAGCGGATCAAGCGTATGC	4565
Db	3705	CGCTCGATGCGATGTTTCGCTTGGTGGTTCGATAGGGCAGGTAGCGGATCAAGCGTATGC	3764
QY	4566	AGCGCGCATTTGCATCAGCCATGATGATATCTTCTCGCAGAGCAGACGTGATGATGAC	4625
Db	3765	AGCGCGCATTTGCATCAGCCATGATGATATCTTCTCGCAGAGCAGACGTGATGATGAC	3824
QY	4626	AGGAGATTCCTCCCCCGGCACTTGCGCCAAATAGCAGCGATTCCTTCCGCTTCAATGACA	4685
Db	3825	AGGAGATTCCTCCCCCGGCACTTGCGCCAAATAGCAGCGATTCCTTCCGCTTCAATGACA	3884
QY	4686	ACGTGAGCAAGCTGGGCGCAAGAAAGCCCGGTGGCGAGCAGATAGCCGCGGTGCC	4745
Db	3885	ACGTGAGCAAGCTGGGCGCAAGAAAGCCCGGTGGCGAGCAGATAGCCGCGGTGCC	3944
QY	4746	TGCTTCGAGATTGATTCAGGGCACAACGAGTCGCTCTTTCGACAAAAGAACCGGGCGC	4805
Db	3945	TGCTTCGAGATTGATTCAGGGCACAACGAGTCGCTCTTTCGACAAAAGAACCGGGCGC	4004
QY	4806	CCCTGCGGTGACAGCCGGAACAACGCGCGCATCAGAGCAGCGCATTCGTGTTGGCCAG	4865
Db	4005	CCCTGCGGTGACAGCCGGAACAACGCGCGCATCAGAGCAGCGCATTCGTGTTGGCCAG	4064
QY	4866	TCATAGCCGAATAGCTCTTCCACCCCAAGCGGCGCGGAGAACTTCGCTGTCATTCATCTTGT	4925
Db	4065	TCATAGCCGAATAGCTCTTCCACCCCAAGCGGCGCGGAGAACTTCGCTGTCATTCATCTTGT	4124
QY	4926	TCATTCATGCGAAACGATTCCTCATCTGTCTCTTTCATCAGATCTTTCGATCCCTCGGCGCAT	4985
Db	4125	TCATTCATGCGAAACGATTCCTCATCTGTCTCTTTCATCAGATCTTTCGATCCCTCGGCGCAT	4184
QY	4986	CAG 4988	
Db	4185	CAG 4187	
RESULT 8			
ADT5136			
ID ADT5136 standard; DNA; 4293 BP.			
XX AC ADT5136;			
XX DT 30-DEC-2004 (first entry)			
XX			

DE Nucleotide sequence of expression vector pMB1-HA-MnSOD.
XX Ophthalmological; radiation; free radical; superoxide anion;
KW heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;
KW glutathione peroxidase 4; GPX-4; gamma glutamyl transpeptidase;
KW xeroderma; xerophthalmia; autoimmune disorder; Sjogren's syndrome;
KW graft-versus-host disease; systemic lupus erythematosus;
KW rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
KW psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.
XX Homo sapiens.
OS Simian virus 40.
OS Synthetic.
XX Key Location/Qualifiers
FH CDS 2..781
FT /tag= a
FT /note= "human Manganese superoxide dismutase cDNA"
FT intron 332..497
FT /tag= b
FT /note= "human beta-globin intron"
FT polyA_signal 347..503
FT /tag= c
FT /note= "SV40 late gene polyadenylation signal"
FT promoter 471..1162
FT /tag= d
FT /note= "CMV promoter"
FT rep_origin 1158..1825
FT /tag= e
FT /note= "ColE1 ori from pBluescript SK+"
FT CDS 1226..2020
FT /tag= f
FT /gene= "kanamycin resistance gene"
XX WO2004087873-A2.
PN 14-OCT-2004.
XX 26-MAR-2004; 2004WO-US009194.
PP 26-MAR-2004; 2004US-0458793P.
PR 26-MAR-2004; 2003US-0458793P.
PR 25-MAR-2004; 2004US-07778889.
XX (GENT-) GENTERIC INC.
PA Bennett MJ, Chen Y;
PI WPI; 2004-737685/72.
DR Attenuating increases in concentrations of radiation-induced free
XX radicals in a mammalian cell, comprises contacting the cell with one or
PT more nucleic acids encoding proteins that neutralizes or eliminates a
PT portion of free radicals.
XX Claim 34; SEQ ID NO 2; 58bp; English.
XX The specification describes a method for attenuating increases in
XX concentrations of radiation-induced free radicals, superoxide anions or
XX heavy metal cations in a mammalian cell. The method comprises contacting
XX the cell with one or more nucleic acids encoding one or more proteins
XX that are expressed in the cell and that neutralizes or eliminates a
XX portion of the free radicals, superoxide anions or heavy metal cations in
XX the cell. The proteins are selected from metallothionein, superoxide
XX dismutase, catalase, glutathione peroxidase (GPX)-4, or gamma glutamyl
XX transpeptidase. The method is useful for attenuating increases in
XX concentrations of radiation-induced free radicals, superoxide anions or
XX heavy metal cations in a mammalian cell, and ameliorating symptoms of
XX xeroderma or xerophthalmia associated with conditions such as autoimmune
XX disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus
XX erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic
XX dysfunction, conditions affecting the CNS, psychogenic disorder, trauma,
XX hepatitis C, cancer and decrease in mastication. The present sequence
XX represents an expression vector used in the method of the invention to

CC express the relevant proteins.
XX
XX Sequence 4293 BP; 1089 A; 1090 C; 1112 G; 1001 T; 0 U; 1 Other;
SQ
Query Match 32.1%; Score 1697.8; DB 13; Length 4293;
Best Local Similarity 86.7%; Pred. No. 1.5e-248;
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;
QY 2706 CTAGACGTAATCATGCTCTACCTGTTCCCTGTGAAATTGTATCCGCTACAAATCC 2765
DB 2212 CTTGGGCTATATCATGCTCTACCTGTTCCCTGTGAAATTGTATCCGCTACAAATCC 2271
QY 2766 ACACAACTATACGAGCGGAGAGCATTAAGTAAAGCTGGGCTCTATATGATGAGCTA 2825
DB 2272 ACACAACTATACGAGCGGAGAGCATTAAGTAAAGCTGGGCTCTATATGATGAGCTA 2331
QY 2826 ACTGACATTAATTTGCGTTGCGCTCACTGCGCGCTTTCCAGTGGGAAACCTGCTGCTCA 2885
DB 2332 ACTGACATTAATTTGCGTTGCGCTCACTGCGCGCTTTCCAGTGGGAAACCTGCTGCTCA 2391
QY 2886 GCTGCACTTAATGAAATGCGCAACGCGCGGAGAGCGGTTGCGATTTGGCGCTCTTC 2945
DB 2392 GCTGCACTTAATGAAATGCGCAACGCGCGGAGAGCGGTTGCGATTTGGCGCTCTTC 2451
QY 2946 CGCTTCCTGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3005
DB 2452 CGCTTCCTGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2511
QY 3006 TCACTGAAAGGCGGTAAATACGTTATCCCAAAATCAAGGGATACGAGGAAAGAAACAT 3065
DB 2512 TCACTGAAAGGCGGTAAATACGTTATCCCAAAATCAAGGGATACGAGGAAAGAAACAT 2571
QY 3066 GTGAGCAAAAGGCGAGCAAAAGGCGAGAAACGTTAAAGGCGGCTGCTGCGCTTTT 3125
DB 2572 GTGAGCAAAAGGCGAGCAAAAGGCGAGAAACGTTAAAGGCGGCTGCTGCGCTTTT 2631
QY 3126 CCATAGGCTCCGCGCCCTGACGAGCATCAAAATTCAGCGTCAAGTCAAGGTGGCG 3185
DB 2632 CCATAGGCTCCGCGCCCTGACGAGCATCAAAATTCAGCGTCAAGTCAAGGTGGCG 2691
QY 3186 AAACCCGACAGGACTTAAAGATACAGAGGCTTCCCGTGAAGGCTCCCTGCGCTC 3245
DB 2692 AAACCCGACAGGACTTAAAGATACAGAGGCTTCCCGTGAAGGCTCCCTGCGCTC 2751
QY 3246 TCCGTTCGACCCCTGCGCTTACCGGATACCTGTCCGCTTCTCCTTGGGAAAGCT 3305
DB 2752 TCCGTTCGACCCCTGCGCTTACCGGATACCTGTCCGCTTCTCCTTGGGAAAGCT 2811
QY 3306 GCGGCTTCTCATAGCTCACGCTGTAGGTATCTCACTGCTGGGTAGTGGTTCGCTCCA 3365
DB 2812 GCGGCTTCTCATAGCTCACGCTGTAGGTATCTCACTGCTGGGTAGTGGTTCGCTCCA 2871
QY 3366 GCTGGGCTGTGTGACGAAACCCCGCTTACGCCGAGCCGCTGTATCCGGTAACTA 3425
DB 2872 GCTGGGCTGTGTGACGAAACCCCGCTTACGCCGAGCCGCTGTATCCGGTAACTA 2931
QY 3426 TCGCTTTGATCCCAACCCCGGTAAAGACACGATTATCGCACTTGACAGCCACTGGTAA 3485
DB 2932 TCGCTTTGATCCCAACCCCGGTAAAGACACGATTATCGCACTTGACAGCCACTGGTAA 2991
QY 3486 CAGGATTAGCAGAGCGAGGTATGTAGCCGCTGTACAGAGTTTGAAGGTGGGCTTA 3545
DB 2992 CAGGATTAGCAGAGCGAGGTATGTAGCCGCTGTACAGAGTTTGAAGGTGGGCTTA 3051
QY 3546 CTACGGCTACACTAGAGAACAGATTTGTATCTGCTCTGCTAGGCAAGCTTACCTT 3605
DB 3052 CTACGGCTACACTAGAGAACAGATTTGTATCTGCTCTGCTAGGCAAGCTTACCTT 3111
QY 3606 CGGAAAAAGGTTGATGCTTTGATCGGCAACCAACCGCTGTGTAGCGGTGTT 3665
DB 3112 CGGAAAAAGGTTGATGCTTTGATCGGCAACCAACCGCTGTGTAGCGGTGTT 3171
QY 3666 TTTTGTTCAGAGCAGAGATTACGCGCAAAAAAGATCTCAAGAAATCTTTGAT 3725

Db	3172	TTTTTTTTCGACGACGAGATTACCGCGCAGGAAAAAAAAAGGATCTCAAGAAATCTTTGAT	3231
Qy	3726	CTTTTCTACGGGGTCTGACGCTCACTGGAACGAAACTCACGTTAAGGATTTTGGTCA	3785
Db	3232	CTTTTCTACGGGGTCTGACGCTCACTGGAACGAAACTCACGTTAAGGATTTTGGTCA	3299
Qy	3786	GAGATTATCTGCACCAAGCGGCATGTCCTCCCACTCTCGAATTGGGGGCAATG	3845
Db	3292	GAG-----	3294
Qy	3846	GATCGCGGGAATAGCGGCTGCTGTTTCCGATGCGACGATTTGCACTGCGGGTAGA	3905
Db	3295	-----	3294
Qy	3906	CTCCGCGAGTCTGTCAGCTTCAGGCGACGACTGAACCACTCGCGAGGGGATCGAGCCC	3965
Db	3295	-----CGGATACATATTATTGAAATGATTTAGAAAAATAACAAATATG	3333
Qy	3966	GGGTTGGCGGAAGAACTCCAGCATAGATCCCGCGCTGGAGAGATCATCGACCGGCGT	4025
Db	3336	GGTTTCCCGGCACATTTCCCGAAAGTGCACCTGTATCGGTTGAAATCCGACAG	3399
Qy	4026	CCGAAAAAGATTCCGAGCCCAACTTTCAAGAAAGCGGGGTGGGATCGAAATCTCG	4085
Db	3396	ATGCGTAAGAGAAAAATACCGGATAGGAAATTTGTAACGTTAAATAT-----	3443
Qy	4086	TGATGGCAGTTGGGCGTCTGCTGGTCCGTCAATTCGAACCCCAAGTCCCGCTCAGAA	4145
Db	3444	-----TAAAGG	3455
Qy	4146	AACTTGTCAGAAAGCGGATAGAAAGCGATGCGCTCGCATCGGAGCGGCGATACCTGTA	4205
Db	3451	AACTTGTCAGAAAGCGGATAGAAAGCGGATGCGCTCGCATCGGAGCGGCGATACCTGTA	3510
Qy	4206	AGCAGAGAAAGCGGTCAAGCCATTCGCGCGCCAACTCTTCAGCAATATCACGGGTACG	4265
Db	3511	AGCAGAGAAAGCGGTCAAGCCATTCGCGCGCCAACTCTTCAGCAATATCACGGGTACG	3570
Qy	4266	AACGCTATGTCCTGATTAACGGGTCCGCGCACACCCAGCGGCGCATGCTGATGATCCAGA	4325
Db	3571	AACGCTATGTCCTGATTAACGGGTCCGCGCACACCCAGCGGCGCATGCTGATGATCCAGA	3633
Qy	4326	AAGCGGCATTTTCCACCATGATATTTCCGCAAGCAGGAGTCGCCATGGGTCAACGAGA	4385
Db	3631	AAGCGGCATTTTCCACCATGATATTTCCGCAAGCAGGAGTCGCCATGGGTCAACGAGA	3690
Qy	4386	TCTTCGCGGTGGGGATATGCGGCTTTGAGCTGGGGAACGTTGGCTGGGCGCAGCCCC	4445
Db	3691	TCTTCGCGGTGGGGATATGCGGCTTTGAGCTGGGGAACGTTGGCTGGGCGCAGCCCC	3750
Qy	4446	TGATGCTCTTGCATGATCATCTCGATCGACAAACCGGGCTTCATCCGAGTACGTCT	4505
Db	3751	TGATGCTCTTGCATGATCATCTCGATCGACAAACCGGGCTTCATCCGAGTACGTCT	3810
Qy	4506	CGCTCGATGCATGTTTTCGCTTGGTGTGATGAGGCGAGTATAGCCGATTCAGCGTATG	4565
Db	3811	CGCTCGATGCATGTTTTCGCTTGGTGTGATGAGGCGAGTATAGCCGATTCAGCGTATG	3870
Qy	4566	AGCGCGCGCATTTGCATCAAGCCATGATGATATCTTTCGGCAGAGCAAGTGAATGAC	4625
Db	3871	AGCGCGCGCATTTGCATCAAGCCATGATGATATCTTTCGGCAGAGCAAGTGAATGAC	3930
Qy	4626	AGGAGATCTGCGCGGACATTTCCGCAATGACGACGATCCCTTCCGCGTTCAAGTGA	4685
Db	3931	AGGAGATCTGCGCGGACATTTCCGCAATGACGACGATCCCTTCCGCGTTCAAGTGA	3990
Qy	4686	ACGTCGACACAGCTGCGCAAGAAAGCGCGCTGTGGCACAACGATAGCGCGCTGCC	4745
Db	3991	ACGTCGACACAGCTGCGCGCAAGAAAGCGCGCTGTGGCACAACGATAGCGCGCTGCC	4050
Qy	4746	TGCTCTGCAGTTCAATTCAAGGACCGGACAGGTGCTCTTGAACAAAAGAAACCGGCGC	4805

Db	4051	TCGCTTTGACATGTTCAATTAGAGGACACCGACAGAGTCGATGCTTGGACAAAAAGAACCGGGCGC	4117
Qy	4806	CCCTGCGCTGACAGCGCGGAGACACGGCGGCATCAGAGCAGCCGATTTGTCTGTTGGCCAG	4865
Db	4111	CCCTGCGCTGACAGCGCGGAGACACGGCGGCATCAGAGCAGCCGATTTGTCTGTTGGCCAG	4170
Qy	4866	TCATGACCGGAATAGCTCTTCCACCCAGCGGCGGAGAACTCGCTGCATATCCATCTTGT	4925
Db	4171	TCATGACCGGAATAGCTCTTCCACCCAGCGGCGGAGAACTCGCTGCATATCCATCTTGT	4230
Qy	4926	TCATATCATGCGAAACGATCCTCATCTGTCCTTGGATGCAGATCTTGAATCCCTCGGCCAT	4985
Db	4231	TCATATCATGCGAAACGATCCTCATCTGTCCTTGGATGCAGATCTTGAATCCCTCGGCCAT	4290
Qy	4986	CAG 4988	
Db	4291	CAG 4293	
RESULT 9			
ID	ADT55135	ADT55135 standard; DNA; 4332 BP.	
XX	ADT55135;		
DT	30-DEC-2004	(first entry)	
XX			
DE	Nucleotide sequence of expression vector pMB1-MnSD.		
XX			
KM	Ophthalmological; radiation; free radical; superoxide anion;		
KM	heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;		
KM	glutathione peroxidase 4; GPx-4; gamma glutamyl transpeptidase;		
KM	xeroderma; xerophthalmia; autoimmune disorder; Sjogren's syndrome;		
KM	griest-virus-host disease; systemic lupus erythematosus;		
KM	rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;		
XX	psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.		
OS	Homo sapiens.		
OS	Simian virus 40.		
XX	Synthetic.		
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Key	Location/Qualifiers		
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XX			
XX	WO2004087873-A2.		
XX			
XX	14-OCT-2004.		
XX			
XX	26-MAR-2004; 2004WO-US009194.		
XX			
XX	26-MAR-2003; 2003US-0458793P.		
XX			
XX	25-MAR-2004; 2004US-07778889.		
XX			
XX	(GENT-) GENTERIC INC.		
XX			
XX	Bennett MJ, Chen Y,		
XX	PI		

```
XX WPI; 2004-737685/72.
XX
XX Attenuating increases in concentrations of radiation-induced free
PT radicals in a mammalian cell, comprises contacting the cell with one or
PT more nucleic acids encoding proteins that neutralizes or eliminates a
PT portion of free radicals.
XX
XX Claim 34; SEQ ID NO 1; 58bp; English.
XX
CC The specification describes a method for attenuating increases in
CC concentrations of radiation-induced free radicals, superoxide anions or
CC heavy metal cations in a mammalian cell. The method comprises contacting
CC the cell with one or more nucleic acids encoding one or more proteins
CC that are expressed in the cell and that neutralizes or eliminates a
CC portion of the free radicals, superoxide anions or heavy metal cations in
CC the cell. The proteins are selected from metallothionein, superoxide
CC dismutase, catalase, glutathione peroxidase (GPx)-4, or gamma glutamyl
CC transpeptidase. The method is useful for attenuating increases in
CC concentrations of radiation-induced free radicals, superoxide anions or
CC heavy metal cations in a mammalian cell, and ameliorating symptoms of
CC xeroderma or xerophthalmia associated with conditions such as autoimmune
CC disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus
CC erythematosus, rheumatoid arthritis, HIV-1 infection, aging, autonomic
CC dysfunction, conditions affecting the CNS, psychogenic disorder, trauma,
CC hepatitis C, cancer and decrease in mast cell function. The present sequence
CC represents an expression vector used in the method of the invention to
CC express the relevant proteins.
XX
SQ Sequence 4332 BP; 1094 A; 1102 C; 1137 G; 998 T; 0 U; 1 Other;
Query Match 32.1%; Score 1697.8; DB 13; Length 4332;
Best Local Similarity 86.7%; Pred. No. 1.5e-248;
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;
QY 2706 CTGAGCATATCATGTCATAGTCTGTTCTCTGTGTAATTTGTTATCCGCTCAATTC 2765
DB 2251 CTGGGGTAAATCATGTCATAGTCTGTTCTCTGTGTAATTTGTTATCCGCTCAATTC 2310
QY 2766 ACACAAATATCGAGCGGAGAGCATAAAGTAAAGCCCTGGGGGCGCTAAAGATGAGCTA 2825
DB 2311 ACACAAATATCGAGCGGAGAGCATAAAGTAAAGCCCTGGGGGCGCTAAAGATGAGCTA 2370
QY 2826 ACTCAATTAATTCGTTGCGTCACTGCGCGCTTTCAGTCGGGAAACCTGTCGAGCA 2885
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DB 2431 GCTGCATTAATGATGCGCAACGCGGGGAGAGGCGGTTTCGTAATGGGCGCTTTC 2490
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DB 2491 CGCTTCCTGCTCACTGACTGCTGCTGCGCTGCTGCTTCGCTGCGGCGAGCGGTATCAG 2550
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DB 2731 AAACCCGACAGACTATAAGATACAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTC 2790
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DB 3271 CTTTCTACGGGCTGACGCTCAGTGAAGAAACACTCAGCTTAAGGATTTGGTCAAT 3330
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 AC ADT55137;
 DT 30-DEC-2004 (first entry)
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 XX
 KW Ophthalmological; radiation; free radical; superoxide anion;
 KW heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;
 KW glutathione peroxidase 4; GPx-4; gamma glutamyl transpeptidase;
 KW xeroderma; xerophthalmia; autoimmune disorder; Sjogren's syndrome;
 KW graft-versus-host disease; systemic lupus erythematosus;
 KW rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
 KW psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.
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 OS Simian virus 40.
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FT FT /*tag= b
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 XX
 PD 14-OCT-2004.
 XX
 PP 26-MAR-2004; 2004MO-US009194.
 XX
 PR 26-MAR-2003; 2003US-0458793P.
 PR 25-MAR-2004; 2004US-07778889.
 XX
 PA (GENT-) GENTERIC INC.
 XX
 PI Bennett MJ, Chen Y;
 XX
 DR WPI; 2004-737685/72.
 XX
 PT Attenuating increases in concentrations of radiation-induced free
 PT radicals in a mammalian cell, comprises contacting the cell with one or
 PT more nucleic acids encoding proteins that neutralizes or eliminates a
 PT portion of free radicals.
 XX
 PS Claim 34; SEQ ID NO 3; 58bp; English.
 XX
 CC The specification describes a method for attenuating increases in
 CC concentrations of radiation-induced free radicals, superoxide anions or
 CC heavy metal cations in a mammalian cell. The method comprises contacting
 CC the cell with one or more nucleic acids encoding one or more proteins
 CC that are expressed in the cell and that neutralizes or eliminates a
 CC portion of the free radicals, superoxide anions or heavy metal cations in
 CC the cell. The proteins are selected from metallothionein, superoxide
 CC dismutase, catalase, glutathione peroxidase (GPx)-4, or gamma glutamyl
 CC transpeptidase. The method is useful for attenuating increases in
 CC concentrations of radiation-induced free radicals, superoxide anions or
 CC heavy metal cations in a mammalian cell, and ameliorating symptoms of
 CC xeroderma or xerophthalmia associated with conditions such as autoimmune
 CC disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus
 CC erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic
 CC dysfunction, conditions affecting the CNS, psychogenic disorder, trauma,
 CC hepatitis C, cancer and decrease in mastication. The present sequence
 CC represents an expression vector used in the method of the invention to
 CC express the relevant proteins.
 XX
 SQ Sequence 5753 BP; 1479 A; 1416 C; 1418 G; 1440 T; 0 U; 0 Other;
 QY Query Match 32.1%; Score 1697.8; DB 13; Length 5753;
 Db Best local similarity 86.7%; Pred. No. 1.5e-248;
 Db Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;
 QY 2706 CTAGACGTAATCATGTCATAGCTGTTTCTGTGTGAATTTGTATCCGCTCACAAATTC 2765
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AC ADT55138;
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XX
DT 30-DEC-2004 (first entry)
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XX Nucleotide sequence of expression vector pMB1-MtLocAT.
XX
XX Ophthalmological; radiation; free radical; superoxide anion;
KW heavy metal cation; metallochionein; superoxide dismutase; SOD; catalase;
KW glutathione peroxidase 4; GPx-4; gamma glutamyl transpeptidase;
KW xerostomia; xerophthalmia; autoimmune disorder; Sjogren's syndrome;
KW graft-versus-host disease; systemic lupus erythematosus;
KW rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
KW psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.
XX
XX Homo sapiens.
OS Simian virus 40.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH intron 332..497
FT /tag= a
FT /note= "human beta-globin intron"
FT polyA_signal 345..503
FT /tag= b
FT /note= "SV40 late gene polyadenylation signal"
FT promoter 471..1162
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XX W02004087873-A2.
XX
XX 14-OCT-2004.
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XX 26-MAR-2004; 2004WO-US009194.
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XX 26-MAR-2003; 2003US-0458793P.
XX 25-MAR-2004; 2004US-07778889.
XX
XX (GENT-) GENTERIC INC.
XX
XX Bennett MJ, Chen Y;
XX
XX WPI; 2004-737685/72.
XX
XX
XX Attenuating increases in concentrations of radiation-induced free
PT radicals in a mammalian cell, comprises contacting the cell with one or
PT more nucleic acids encoding proteins that neutralizes or eliminates a
PT portion of free radicals.
XX
XX Claim 34; SEQ ID NO 4; 58pp; English.
XX
XX The specification describes a method for attenuating increases in
CC concentrations of radiation-induced free radicals, superoxide anions or
CC heavy metal cations in a mammalian cell. The method comprises contacting
CC the cell with one or more nucleic acids encoding one or more proteins
CC that are expressed in the cell and that neutralizes or eliminates a
CC portion of the free radicals, superoxide anions or heavy metal cations in

CC the cell. The proteins are selected from metallothionein, superoxide
CC dismutase, catalase, glutathione peroxidase (GPx)-4, or gamma glutamyl
CC transpeptidase. The method is useful for attenuating increases in
CC concentrations of radiation-induced free radicals, superoxide anions or
CC heavy metal cations in a mammalian cell, and ameliorating symptoms of
CC xerostomia or xerophthalmia associated with conditions such as autoimmune
CC disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus
CC erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic
CC dysfunction, conditions affecting the CNS, psychogenic disorder, trauma,
CC hepatitis C, cancer and decrease in mastication. The present sequence
CC represents an expression vector used in the method of the invention to
CC express the relevant proteins.
XX
SQ Sequence 5760 BP; 1471 A; 1422 C; 1426 G; 1441 T; 0 U; 0 Other;
Query Match 32.1%; Score 1697.8; DB 13; Length 5760;
Best Local Similarity 86.7%; Pred. No. 1.5e-248;
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;
QY 2706 CTAGACGTAATCATGTCATGCTGTTTCCGTGTGTAATGTTATCCGCTCACAATTCC 2765
DB 3679 CTTGGCGTAATCATGTCATGCTGTTTCCGTGTGTAATGTTATCCGCTCACAATTCC 3738
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DB 4279 GGCGCTTTCATATGCTCAGCGTGTAGTATTCAGATTCGATGAGTCTGCTCCAA 4338
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RESULT 12
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 KW class IIS restriction endonuclease recognition site;
 KW endogenous mouse promoter element; tissue-specific gene expression;
 KW hormone-specific gene expression; ss;
 KW developmental-specific gene expression.
 XX
 OS Synthetic.
 XX
 PN WO9838326-A1.
 XX
 PD 03-SEP-1998.
 XX
 PF 28-FEB-1998; 98WO-US003918.
 XX
 PR 28-FEB-1997; 97US-0070910P.
 XX
 PA (NATU-) NATURE TECHNOLOGY CORP.
 PI Hodgson CP, Zink MA, Xu G;
 XX
 DR WPI; 1998-495399/42.
 XX
 PT Method for assembling gene or gene vector - comprises use of primers
 containing class IIS restriction endonuclease recognition sites.
 XX
 PS Example 2; Page 107-110; 141pp; English.
 XX
 CC The invention provides a novel method for directing self-assembly of a
 CC gene having three or more fragments in a directionally and spatially
 CC ordered fashion to produce a gene or a gene vector. The method involves
 CC usage of primers, containing class IIS restriction endonuclease
 CC recognition sites, for isolation of these fragments. As described in the
 CC disclosure, the method may also use a vector for the incorporation and
 CC screening of endogenous mouse promoter elements for the identification of

CC cell specific promoters. In the example given, plasmids pBK-CMV
CC (AAV33626), pVLAMB (AAV33623) and pVIOVGH-900 (AAV33621) were used as
CC templates from which six fragments were amplified. Each of the fragments
CC contained different regulatory sequences. The six PCR fragments were
CC designed to self-assemble into a retro-vector using the method of the
CC invention. The present sequence, designated as GENS 981, represents the
CC monomeric DNA sequence of the six ligated fragments. In general, the
CC method is claimed to be useful for isolating and identifying regulatory
CC sequences from a cell, including those for enhanced biological activity,
CC or tissue-specific, hormone-specific or developmental-specific gene
CC expression

XX Sequence 5594 BP; 1232 A; 1519 C; 1518 G; 1325 T; 0 U; 0 Other;

Query Match 31.3%; Score 1652.4; DB 2; Length 5594;

Best Local Similarity 85.4%; Pred. No. 116-241;

Matches 1916; Conservative 0; Mismatches 261; Indels 67; Gaps 4;

Qy 3107 CCGCGTTGCTGGCGCTTTTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGAC 3166
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Qy 3167 GCTCAAGTCAGAGGTGGCGAAACCCGACAGACTATAAAGATCAAGCGCTTTCCCTCG 3226
Db 5531 GCTCAAGTCAGAGGTGGCGAAACCCGACAGACTATAAAGATCAAGCGCTTTCCCTCG 5472
Qy 3227 GAAGCTCCCTGCTGCTCTCTGTTCCGACCTGCGCCCTTAACCGGATACCTGTCGCGCT 3286
Db 5471 GAAGCTCCCTGCTGCTCTCTGTTCCGACCTGCGCCCTTAACCGGATACCTGTCGCGCT 5412
Qy 3287 TTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTGAGGTATCTCAAGTTCCG 3346
Db 5411 TTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTGAGGTATCTCAAGTTCCG 5352
Qy 3347 TGTAGTGTGCTGCTCCAGCTGGCTGTGTGACGAACCCCGCTTCAAGCGCGCT 3406
Db 5351 TGTAGTGTGCTGCTCCAGCTGGCTGTGTGACGAACCCCGCTTCAAGCGCGCT 5292
Qy 3407 GCGGCTTATCCGGTAACTATGCTGTGATGACCAACCGGTTAAGACAGACTATTCGCGAC 3466
Db 5291 GCGGCTTATCCGGTAACTATGCTGTGATGACCAACCGGTTAAGACAGACTATTCGCGAC 5232
Qy 3467 TGGGAGAGCCACTGTGTAACAGATTAGCAGAGGATATGAGCGGTCTACAGAGT 3526
Db 5231 TGGGAGAGCCACTGTGTAACAGATTAGCAGAGGATATGAGCGGTCTACAGAGT 5172
Qy 3527 TCTTGAAGTGTGCTTAACTACGAGCTACCTAGAAAGACAGTATTGTAATCTGCGCTC 3586
Db 5171 TCTTGAAGTGTGCTTAACTACGAGCTACCTAGAAAGACAGTATTGTAATCTGCGCTC 5112
Qy 3587 TGTGGAAGCCAGTTAACTTCCGAAAAAGATTGTAAGTCTTGAATCCGGCAAAACCA 3646
Db 5111 TGTGGAAGCCAGTTAACTTCCGAAAAAGATTGTAAGTCTTGAATCCGGCAAAACCA 5052
Qy 3647 CCGGCTGAGAGGTGGTGTGTTTGTGTTGCAAGCAGACAGATTACGCGAGAAAAGAGAT 3706
Db 5051 CCGGCTGAGAGGTGGTGTGTTTGTGTTGCAAGCAGACAGATTACGCGCGCCGAGTGAAG 4992
Qy 3707 CTCAAGAAAGATCTTGAATCTTGTCTACGGGCTCTGACGCTC-----AGTGAACG 3757
Db 4991 GGTGTGGGCTCTTATATTTAGAGCTCGGGGACAGAAAGCGCGCAACAGAAACGGAAGCG 4932
Qy 3758 AAAAAGCTGTAAGAGATTTTGTGATGAGATTAATGTCGACCAAGAGCGCATCTGTC 3817
Db 4931 AACTGATTTGTTAGTTCAAAATAGGACAGAGGCTATTTCAAGTCTTTGGGGCAACCTTGA 4872
Qy 3818 CTC-----CCACTCTGACAGTTGCGGGGCGATGATGCGGAGTAGCCGCTG 3864
Db 4871 AACTGATTTGTTAGTTCAAAATAGGACAGAGGCTATTTCAAGTCTTTGGGGCAACCTTGA 4812
Qy 3865 CTGCTTTCTGATGAGCGAGCGAGTTGCG-----ACTGCGGATGAACCTCCGCGAG 3914
Db 4811 CTGCGCTTGAAGCGGGGACAGAACTGCTTACCAAGATATCTGTTTGGCCATATTTCA 4752

Qy 3915 GTGCTCAGCTTCAGAGCAGCTGAACCACTGCGGAGGGGATCGAGCCCGGGGTGGGC 3974
Db 4751 GCTGTTTCATCTGTTCTTTGGCCCTGAGCGGGGACAGAACTGCTTACCAAGATATCTG 4692
Qy 3975 GAAGAATCTCAGCATGAGATCCCGCGCTGAGAGATCAACGCGCGGTCCGGAAC 4034
Db 4691 TTTGGCCATATTCAGCGTTCATCTGTTCTGACCTTGAATCGAACTTCTATCTC 4632
Qy 4035 GATTCCGAAGCCCACTTTATAGAAAGCGCGGTGAATCGAAATCTG----- 4085
Db 4631 AGTTATGATTTTTCATGCTTCGCAAAATGCGCTTACTTAAGCTTCCAAACCTA 4572
Qy 4086 -----TGATGCAAGTTTGGCGGTGCGCTTGGCTGAT 4119
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Qy 4120 TCGAACCAGAGTCCGCTTCAGAAACCTGTCAGAAAGCGGATGAGAGCGATGCGCT 4179
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Db 4451 GCGAATGGGAGCGGCGATACCTTAAAGCACAGAGAAAGCGGTACGCCATTCCGCCAA 4392
Qy 4240 GCTCTTCAAGCAATATCAACGGGTAGCCAAAGCTATGCTCTGATAGCGGTCCGCCAACCA 4299
Db 4391 GCTCTTCAAGCAATATCAACGGGTAGCCAAAGCTATGCTCTGATAGCGGTCCGCCAACCA 4332
Qy 4300 GCCCGCACAGTCCAGTAAATCAAGAAAGCGGCAATTTTCCACATGATATTTCCGCAAGC 4359
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Qy 4360 AGGATGCGCATGGGTGTCAGACAGATCTTCGCGGTGGGATGCGCGCTTGAAGCTGG 4419
Db 4271 AGGATGCGCATGGGTGTCAGACAGATCTTCGCGGTGGGATGCGCGCTTGAAGCTGG 4212
Qy 4420 CGAAGCTGGGCTGGGCGAGCGCCCTGATGCTTTCGTCAGATCACTCCGATCGACAA 4479
Db 4211 CGAAGCTGGGCTGGGCGAGCGCCCTGATGCTTTCGTCAGATCACTCCGATCGACAA 4152
Qy 4480 GACCGGCTTCCATCCAGTACGTGCTGCTGATGATGATGTTTGGTGTGATGATG 4539
Db 4151 GACCGGCTTCCATCCAGTACGTGCTGCTGATGATGATGTTTGGTGTGATGATG 4092
Qy 4540 GGCAGTACCGGATCAAGGATGACAGCGCGCGCATTTGATCAACGATGATGATCTT 4599
Db 4091 GGCAGTACCGGATCAAGGATGACAGCGCGCGCATTTGATCAACGATGATGATCTT 4032
Qy 4600 TTTGCGGAGAGCAAGGTGAGATGACAGAGATCTTCCCGGACCTTCCGCAATGCA 4659
Db 4031 TTTGCGGAGAGCAAGGTGAGATGACAGAGATCTTCCCGGACCTTCCGCAATGCA 3972
Qy 4660 GCGAGTCCCTTCCCGCTTCAAGTACAGATGACAGCTGCGCAAGAAAGCGCGTGC 4719
Db 3971 GCGAGTCCCTTCCCGCTTCAAGTACAGATGACAGCTGCGCAAGAAAGCGCGTGC 3912
Qy 4720 TGGCAGCCAGATGAGCGGCTGCTGCTGCTTGTGAGTTCAATTCAGGCAACCGGACAGT 4779
Db 3911 TGGCAGCCAGATGAGCGGCTGCTGCTGCTTGTGAGTTCAATTCAGGCAACCGGACAGT 3852
Qy 4780 CCGTCTTGAAGAAAGAAACCGGGCGCGCCCGCTGACACCGGAAACCGGGCGATCAG 4839
Db 3851 CCGTCTTGAAGAAAGAAACCGGGCGCGCCCGCTGACACCGGAAACCGGGCGATCAG 3792
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Db 3791 AGCAGCCGATTTGTTGTGTCAGATCATAGCGAATAGCTTCCACCAAGCGCGCG 3732
Qy 4900 GAGAACCTGCGTGCATTCATCTTTTGAATCATGCGAAACGATCTCATCTGTCTTT 4959
Db 3731 GAGAACCTGCGTGCATTCATCTTTTGAATCATGCGAAACGATCTCATCTGTCTTT 3672

D 3229 GGGCAACTCCCGCCCGCCGAGTCTGCGGATCTGCTCATGAGCCGCGCCGAGAGCGT 3170
Q 3863 TGTGTGTTCTTGATGCGGACGAGATTGCACTGCGGTAAGAACTCCGAGAGTCTCA 3922
D 3169 CCGGAAATTGTGACACGACCTCCGACCACTCGGCGTACAGCTCTGTCAGGCGCGCA 3110
Q 3923 GCC----- 3925
D 3109 CCGACACCCAGGCGGAGTGTGTCGCGACCACTGCTCTGACCGCGCTGATGACA 3050
Q 3926 ---TCAGGACAGCTGTAACCACTGCGAGAGGATTCAGACCGGGGTTGGCGAAGAACT 3982
D 3049 GGGTACGTCGTCCCGGACCAACCGGAAATGCTCTTCCAGAAAGTCCCGGAGAAC 2990
Q 3983 CCAGCATAGATATCCCGGCTGAGAGATCATCCAGCGCGGCGCCGAAAAAGATTCCGA 4042
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Q 4043 AGCCCAACCTTTCATAGAAAGCGCGGTGAATCGAAATCTGATGCGAGTTGGCG 4102
D 2929 CGGCACTGTCATCTTGCGCATGTTGGCCCTCTCAGCTGATTAATTGAAGCATTAATC 2870
Q 4103 TCGCTGTGTCGCTCATTTGCAACCCAGAGTCCG----- 4137
D 2869 AGGGTTATTGTCATAGAGCGAATCATATTGATATTGAAAAATAACAATAAG 2810
Q 4138 ----- 4137
D 2809 GGGTCCGCGCACTTCCCGAAAAAGTCCCACTGTATGCGGTGTGAATAACGCAAG 2750
Q 4138 -----CTCAAGAAATC 4150
D 2749 ATGCGTAAGGAAAAATACGCGCATCAGGAATTGTGAAGCTTAATTAATTCAGAAATC 2690
Q 4151 GTCAGAAAGCGATAGAAAGCGATGCGTCCGAATCGGAGCGCGATACCGTAAGCAC 4210
D 2689 GTCAGAAAGCGATAGAAAGCGATGCGTCCGAATCGGAGCGCGATACCGTAAGCAC 2630
Q 4211 GAGGAGCGGTCAAGCCATTCGCGCGCAAGCTCTTCAGCAATATCACGGTTAGCCAC 4270
D 2629 GAGGAGCGGTCAAGCCATTCGCGCGCAAGCTCTTCAGCAATATCACGGTTAGCCAC 2570
Q 4271 TATGCTGATAGAGGTCGCGCACACCGCGCGCACAGTCGATGATCCAGAAAAAG 4330
D 2569 TATGCTGATAGAGGTCGCGCACACCGCGCGCACAGTCGATGATCCAGAAAAAG 2510
Q 4331 GCCATTTTCCACATGATATTTGCGCAAGCAGCATTCGCGATGAGTCAAGAGATCTC 4390
D 2509 GCCATTTTCCACATGATATTTGCGCAAGCAGCATTCGCGATGAGTCAAGAGATCTC 2450
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Q 4451 CTCCTGCTCAGATCATCTGATCGACAAAGACCGGCTTCCATCCGAGTACGTCGCTC 4510
D 2389 CTCCTGCTCAGATCATCTGATCGACAAAGACCGGCTTCCATCCGAGTACGTCGCTC 2330
Q 4511 GATGCGATGTTTGGCTTGATGAAATGGGCAAGTACCGGATCAAGCGTATGACCG 4570
D 2329 GATGCGATGTTTGGCTTGATGAAATGGGCAAGTACCGGATCAAGCGTATGACCG 2270
Q 4571 CCGCATTCGATCAGCCATGATGATCTTTCTCGCGAGAGCAAGGTGAGATGACAGAG 4630
D 2269 CCGCATTCGATCAGCCATGATGATCTTTCTCGCGAGAGCAAGGTGAGATGACAGAG 2210
Q 4631 ATCTGCGCGGCACTTCGCGCAATAGACAGCAGTCCCTTCGCGTCAAGTCAAGATC 4690
D 2209 ATCTGCGCGGCACTTCGCGCAATAGACAGCAGTCCCTTCGCGTCAAGTCAAGATC 2150
Q 4691 GAGCAAGCTGCGCAAGAAACCGCGCTGTTGCGCAGCAGCATAGCCGCTGCTCTC 4750
D 2149 GAGCAAGCTGCGCAAGAAACCGCGCTGTTGCGCAGCAGCATAGCCGCTGCTCTC 2090

Q 4751 CTGAGTTTATTAGGGCAACCGACAGTGGTCTTGAACAAAAAGAACGGGCGCCCTG 4810
D 2089 TTGCAATTCATTAGGGCAACCGACAGTGGTCTTGAACAAAAAGAACGGGCGCCCTG 2030
Q 4811 CGTGAAGCCGGAACAACGGGCGATCAGACAGCCGATTTGTGTGTGCCAGTCA 4870
D 2029 CGTGAAGCCGGAACAACGGGCGATCAGACAGCCGATTTGTGTGTGCCAGTCA 1970
Q 4871 GCCGATATGCTCTTCAACCAAGCGCGGAGAACTGCGTCAATCATTTGTTCAAT 4930
D 1969 GCCGATATGCTCTTCAACCAAGCGCGGAGAACTGCGTCAATCATTTGTTCAAT 1910
Q 4931 CATGCGAAAGATCTCATCTGCTCTTGAATCAGATCTGATTCGCTGCGGCGCATCAT 4990
D 1909 CATGCGAAAGATCTCATCTGCTCTTGAATCAGATCTGATTCGCTGCGGCGCATCAT 1850
Q 4991 CTTGCGCGCAAGAAACCATCCAGTTTACTTTGACAGGCTTCCCACTTACAGAGG 5050
D 1849 CTTGCGCGCGAAGAAACCATCCAGTTTACTTTGACAGGCTTCCCACTTACAGAGG 1790
Q 5051 CGCCCACTGCGCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5110
D 1789 CGCCCACTGCGCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1730
Q 5111 CCATGTAGCCCACTGCAAGTACCTGCTTCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 5170
D 1729 CCATGTAGCCCACTGCAAGTACCTGCTTCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1670
Q 5171 GATAGCCCATGATGATTCATTCGCGGTCAGCAACGTTTCTGCGAAGTCTGCTCTA 5230
D 1669 GATAGCCCATGATGATTCATTCGCGGTCAGCAACGTTTCTGCGAAGTCTGCTCTA 1610
Q 5231 CGTG 5234
D 1609 CGTG 1606

RESULT 14
ADU71288/c
ID ADU71288 standard; DNA; 4245 BP.
XX
AC ADU71288;
XX
AC
XX
DT 06-MAY-2004 (first entry)
XX
DE PCR-BiuntII-TOPO cloning vector containing M13 primers.
XX
KW de; vector; DNA amplification; sequencing; collapsible emulsion.
XX
OS Synthetic.
XX
PN WO200310678-A1.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-AU000746.
XX
PR 13-JUN-2002; 2002AU-00002981.
XX
PA (NUCL-) NUCLEICS PTY LTD.
XX
PI Tillec D, Thomas T;
XX
DR WPI; 2004-191031/18.
XX
PS Disclosure; Fig 1; 11pp; English.
XX
CC The present invention relates to a method of performing a chemical
CC reaction between reactants, which involves subjecting an emulsion
CC comprising a discontinuous first phase in which at least one of the
CC reactants is present, and a continuous second phase, to a physical or
CC chemical change such that a continuous phase is formed from the

Mon May 15 09:36:48 2006

us-09-921-143-36.rng

Page 27

Job time : 1973 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2006, 17:56:56 ; Search time 12708 Seconds
(without alignments)
19450.437 Million cell updates/sec

Title: US-09-921-143-36

Perfect score: 5283

Sequence: 1 aagcttgacctatgcgac...

Scoring table: IDENTITY NUC

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hsc: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gsa1: *
10: gb_gsa2: *
11: gb_gsa3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1008.4	19.1	1186	8	DR045845 FP-10_F08
2	1003.6	19.0	1176	8	CX943193 LamGestG
3	991	18.8	2450	4	AK047844 Mus muscu
4	948	17.9	1067	1	AU081137 AU081137
5	939.4	17.8	954	7	CK283361 CK283361
6	924.6	17.5	947	7	CK298208 CK298208
7	919.8	17.4	1089	1	AU081124 AU081124
8	918.6	17.4	935	7	CK284786 CK284786
9	911	17.2	936	7	CK256977 CK256977
10	907	17.2	910	7	CK287930 CK287930
11	897.4	17.0	1049	10	CL021189 CL021189
12	886.4	16.8	933	7	CK291799 CK291799
13	881	16.7	951	8	CY983341 CY983341
14	875	16.6	925	6	CB886151 Bn01b_02o
15	866.2	16.4	1073	6	CP269652 Fcy1c01d8
16	859.2	16.3	885	10	CL076016 CL076016
17	856.8	16.2	875	8	CX012952 CX012952
18	854	16.2	1191	8	DR045882 DR045882
19	843	16.0	856	7	CK287297 CK287297
20	826	15.6	868	8	CY984340 CY984340
21	820.6	15.5	1025	10	CL021193 CL021193
22	820	15.5	894	8	DN641029 DN641029

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26	809.8	15.3	813	8	CX006605 CX006605
27	809.2	15.3	966	9	B2570738 B2570738
28	805.8	15.3	865	7	CK125894 CK125894
29	803	15.2	804	7	CK291519 CK291519
30	800.4	15.2	804	8	CY979032 CY979032
31	794	15.0	811	7	CK288185 CK288185
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33	792	15.0	810	11	DE097025 DE097025
34	792	15.0	810	11	DE097277 DE097277
35	792	15.0	810	11	DE097360 DE097360
36	792	15.0	810	11	DE097448 DE097448
37	792	15.0	810	11	DE097511 DE097511
38	792	15.0	810	11	DE098632 DE098632
39	792	15.0	810	11	DE099849 DE099849
40	792	15.0	810	11	DE100113 DE100113
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ALIGNMENTS

RESULT 1
LOCUS DR045845 1186 bp mRNA linear EST 02-JUN-2005
DEFINITION FP-10_F08.SPO cDNA library of Phaeosphaeria nodorum grown on wheat cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.

ACCESSION DR045845
VERSION DR045845.1 GI:66909681
KEYWORDS EST.
SOURCE Phaeosphaeria nodorum
ORGANISM Phaeosphaeria nodorum

REFERENCE Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.

AUTHORS Bindschedler,L.V., Cooper,R.M., Thomas,S.W., Madrid,M.P. and Oliver,R.P.
TITLE cDNA library of Phaeosphaeria nodorum grown on wheat cell walls

JOURNAL Unpublished (2005)
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SOUTH STREET, MURDOCH, W.A 6150, AUSTRALIA
TEL: +0893607404
EMAIL: roliver@murdoch.edu.au.

FEATURES
source Location/Qualifiers
1..1186
/organism="Phaeosphaeria nodorum"
/mol_type="mRNA"
/db_xref="taxon:13684"
/clone_lib="cDNA library of Phaeosphaeria nodorum grown on wheat cell walls"

ORIGIN
Query Match 19.1%; Score 1008.4; DB 8; Length 1186;
Best local similarity 99.2%; Pred. No. 1.2e-278; Indels 2; Gaps 2;
Matches 1034; Conservative 0; Mismatches 6;

QY 2711 CGTATCATGTCATAGCTTTCTGTTGAAATTGTATCCGCTCAATTCACACA 2770
DB 23 CGTATCATGTCATAGCTTTCTGTTGAAATTGTATCCGCTCAATTCACACA 82
QY 2771 AACTAGACGCCGGAAGATAAGTGTAAAGCTGGGTGCTATATGATGACATACTCA 2830
DB 83 AACTAGACGCCGGAAGATAAGTGTAAAGCTGGGTGCTATATGATGACATACTCA 142
QY 2831 CATTATTCGTTGCGCTCACTGCCGCTTTCAGTGCAGGAACCTGTGCGACGCTGC 2890

Db 143 CATTAATTTGGCTTGGCTCACTGCGCTTTCAGTGGGAAACCTGTCTGCGACGCTGC 202
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QY 2951 CCTGCGCTCACTGACTCGCTGCGCTCGGTCGTTGCGGCTGCGGCGAGCGGATTCAGCTCACT 3010
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QY 3011 CAAAGGCGGTAAATACGGTTATCCACAGATATGAGGATTAACGCGAGAAAGAAACATGTGAG 3070
Db 323 CAAAGGCGGTAAATACGGTTATCCACAGATATGAGGATTAACGCGAGAAAGAAACATGTGAG 382
QY 3071 CAAAGGCGGTAAATACGGTTATCCACAGATATGAGGATTAACGCGAGAAAGAAACATGTGAG 3130
Db 383 CAAAGGCGGTAAATACGGTTATCCACAGATATGAGGATTAACGCGAGAAAGAAACATGTGAG 442
QY 3131 GGCCTCCGCGCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGCGAAACC 3190
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QY 3191 CGACAGACTATTAAGATACCAAGGCGTTTCCCGCTGAGAGCTCCCTGTCGCTCTCTG 3250
Db 503 CGACAGACTATTAAGATACCAAGGCGTTTCCCGCTGAGAGCTCCCTGTCGCTCTCTG 562
QY 3251 TTCCGACCTGCGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGAAGCGGTGCGC 3310
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QY 3311 TTTCTCATAGCTACGCTGTAGATATCTCAGTTTCGAGTTCAGTTCGTTGCTCCAAAGCTG 3370
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QY 3371 GGTGTGAGAGGAAACCCCGCTTTCAGCCGAGCGCTGCGCTTATCCGTAATCTATGCTC 3430
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QY 3491 TTGAGAGAGCGGATATGAGCGGCTGCTACAGATTTCTTGAAGGTGGGCTTAACTAAG 3550
Db 803 TTGAGAGAGCGGATATGAGCGGCTGCTACAGATTTCTTGAAGGTGGGCTTAACTAAG 862
QY 3551 GCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAA 3610
Db 863 GCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAA 922
QY 3611 AAAGAGTTGTAAGTCTTGTATCCGCAAAACCAACGCGTGTAGCGGTGTTTTTTT 3670
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QY 3671 TTGCAAGAGAGAGATTACGCGCAAGAAAGAAAGATCTCAAGAAATCTTGTATCTTT 3730
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QY 3731 CTACGCGGTCTGACGCTCAGTG 3752
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RESULT 2
CX943193 1176 bp mRNA linear EST 09-FEB-2005
LOCUS LamJestG8 Laminaria japonica Lambda Zap Express Library Laminaria
DEFINITION japonica cDNA 5', mRNA sequence.
ACCESSION CX943193
VERSION CX943193.1 GI:58802440
KEYWORDS EST.
SOURCE Laminaria japonica

ORGANISM Laminaria japonica
Eukaryota; stramenopiles; Phaeophyceae; Laminariales;
Laminariaceae; Laminaria.
REFERENCE 1 (bases 1 to 1176)
AUTHORS Xuan,J., Zhao,G., Wang,W., Duan,D., Weng,M. and Wang,B.
TITLE Expressed sequence tag analysis of the brown alga Laminaria japonica (Phaeophyceae)
JOURNAL Unpublished (2005)
COMMENT Contact: Xuan JS
The State Key Laboratory of Plant Genome Research
Institute of Genetics and Developmental Biology, Chinese Academy of Science
Dacun Road, Chaoyang District, Beijing, China, 100101
Tel: 086 010 64889353
Fax: 086 010 64873428
Email: bnuxuan@hotmail.com
Seq primer: T3 Forward
High quality sequence stop: 1176.
Location/Qualifiers
FEATURES
source
1..1176
/organism="Laminaria japonica"
/mol_type="mRNA"
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/clone_1b="Laminaria japonica Lambda Zap Express Library"
/note="Vector: Uni-ZAP® XR vector; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 19.0%; Score 1003.6; DB 8; Length 1176;
Best local Similarity 98.4%; Pred. No. 2.8e-277;
Matches 1067; Conservative 0; Mismatches 9; Indels 8; Gaps 5;
QY 2711 CGTAATCATGCTATGCTGTTTCTGCTGTGAAATTTGTTATCCGTCGAATTCACACA 2770
Db 37 CGTAATCATGCTATGCTGTTTCTGCTGTGAAATTTGTTATCCGTCGAATTCACACA 96
QY 2771 ACATACGAGCGGAAACATTAAGTGTAAAGCTGAGGATGCTTATAGTAGTAACTCA 2830
Db 97 ACATACGAGCGGAAACATTAAGTGTAAAGCTGAGGATGCTTATAGTAGTAACTCA 156
QY 2831 CATTAATGCGTTCGCTCACTGCCCCCTTTTCAAGTCGAGAAACCTGTGTGCCAGCTGC 2890
Db 157 CATTAATGCGTTCGCTCACTGCCCCCTTTTCAAGTCGAGAAACCTGTGTGCCAGCTGC 216
QY 2891 ATTAAATGAATCGGCCCAACCGCGGGGAGAGGCGGTTTGCTATTGGGCGCTCTTCGCTT 2950
Db 217 ATTAAATGAATCGGCCCAACCGCGGGGAGAGGCGGTTTGCTATTGGGCGCTCTTCGCTT 276
QY 2951 CCTGCTCACTGACTCGCTGCGCTCGGTGCTTGGCTGCGGAGCGGATACACTCACT 3010
Db 277 CTTGCTCACTGACTCGCTGCGCTCGGTGCTTGGCTGCGGAGCGGATACACTCACT 336
QY 3011 CAAAGGCGGTAAATACGGTTATCCACAGATATGAGGATTAACGAGAAAGAAACATGTAG 3070
Db 337 CAAAGGCGGTAAATACGGTTATCCACAGATATGAGGATTAACGAGAAAGAAACATGTAG 396
QY 3071 CAAAGGCGGTAAAGGCGGAGAACCGTAAAGGCGGTTGCTGAGGCTTTTTCATA 3130
Db 397 CAAAGGCGGTAAAGGCGGAGAACCGTAAAGGCGGTTGCTGAGGCTTTTTCATA 456
QY 3131 GGCCTCCGCGCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGCGAAACC 3190
Db 457 GGCCTCCGCGCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGCGAAACC 516
QY 3191 CGACAGACTATTAAGATACCAAGGCGTTTCCCGTGAAGCTCCCTGACGCTCTCTG 3250
Db 517 CGACAGACTATTAAGATACCAAGGCGTTTCCCGTGAAGCTCCCTGACGCTCTCTG 576
QY 3251 TTCCGACCTGCGCTTACCGGATACCTGTCGCTTTTCTCCCTTCGGAAGCGTGGCG 3310
Db 577 TTCCGACCTGCGCTTACCGGATACCTGTCGCTTTTCTCCCTTCGGAAGCGTGGCG 636

QY	3311	TTTCTCATAGCTCAAGCTGATGATCTCACTTCGCTGATGATGCTGCTGCTCAAGCTGG	3370
Db	637	TTTCTCATAGCTCAAGCTGATGATCTCACTTCGCTGATGATGCTGCTGCTCAAGCTGG	696
QY	3371	GCTGTGTCAGAAACCCCGCTTACGCGGACCGCTGCGCTTATCCGTAACATATGCTC	3430
Db	697	GCTGTGTCAGAAACCCCGCTTACGCGGACCGCTGCGCTTATCCGTAACATATGCTC	756
QY	3431	TTGAGTCCACCCGGTAAAGACGATGATGCGGACCTGAGGACGACCTGTAACAGGA	3490
Db	757	TTGAGTCCACCCGGTAAAGACGATGATGCGGACCTGAGGACGACCTGTAACAGGA	816
QY	3491	TTGAGTCCACCCGGTAAAGACGATGATGCGGACCTGAGGACCTGTAACAGGA	3550
Db	817	TTGAGTCCACCCGGTAAAGACGATGATGCGGACCTGAGGACCTGTAACAGGA	876
QY	3551	GCTACACTAGAAAGACGATGATGCGGACCTGAGGACCTGTAACAGGA	3610
Db	877	GCTACACTAGAAAGACGATGATGCGGACCTGAGGACCTGTAACAGGA	936
QY	3611	AAAGAGTTGATGCTTGTATCGGCAAGAAACACCGCTGATGCTGCTTTTGG	3670
Db	937	AAAGAGTTGATGCTTGTATCGGCAAGAAACACCGCTGATGCTGCTTTTGG	995
QY	3671	TTTGCAAGCAGCAGATTAACGCGAGAAAGATCTCAGAGATCTTGTATCTTT	3730
Db	996	TTTGCAAGCAGCAGATTAACGCGAGAAAGATCTCAGAGATCTTGTATCTTT	1053
QY	3731	CTACGGGCTGACGCTGATGAGCAAGAACTCAGCTTAAAGATTTTGTATGAGAT	3790
Db	1054	CTACGGGCTGACGCTGATGAGCAAGAACTCAGCTTAAAGATTTTGTATGAGAT	1108
QY	3791	TATC 3794	
Db	1109	TATC 1112	
RESULT 3	AK047844		
LOCUS	AK047844		
DEFINITION	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:CI30004M09 product:vascular endothelial growth factor C, full insert sequence.		
ACCESSION	AK047844	GI:26339001	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)		
REFERENCE	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komano, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)		
JOURNAL	11042159		
PUBMED			
REFERENCE	3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Komano, H., Akiyama, J., Nishi, K., Kikunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Itonaka, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format		

JOURNAL	11076861		
PUBMED			
REFERENCE	4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)		
JOURNAL			
REFERENCE	5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)		
JOURNAL			
REFERENCE	6 (bases 1 to 2450)		
AUTHORS	Adachi, J., Aizawa, K., Akiyama, T., Arahata, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komano, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.		
JOURNAL			
REFERENCE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/		
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	/dev_stage="16 days embryo"		
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ORIGIN	Query Match 18.8%; Score 991; DB 4; Length 2450; Best Local Similarity 85.4%; Pred. No. 1.6e-273;		

Matches 1121; Conservative 0; Mismatches 180; Indels 12; Gaps 1;			
Qy	481	CACCTGGGTTGGATGATCATCATGACATCGCTGGGCTTCTCTCTGCTGGCTGTTCT	540
Db	151	CTCCCTCTCCCGATCCATCCATGACATGCTGTGTCTGTCTGTCTGTCTGTCTTC	210
Qy	541	CTGCTGCGCGCTGGCTGTCTCCCGGTCCTGCGAGGCGCGCGCGCGCGCGCTTC	600
Db	211	CTGCTGCGCGCTGGCTGTATCCCGATCCGCGAGGCGCGCGCGCGCGCGCTTC	270
Qy	601	GAGTCCGAGATCTCACTCTGCGAGCGCGAGCCGAGCGCGGTGAGCCGCTTATGCA	660
Db	271	GAGTCCGAGATCTGAGCTTCTGCGAGCGCGAGCCGAGCGCGGTGAGCCGCTTATGAA	330
Qy	661	AGCAAGATCTGAGGAGGAGTTACGCTGTGTGCACTGATGATGCAATCATGACTGTA	720
Db	331	GGCAAGATCTGAGGAGGAGTTGAGCTGTGTGCACTGATGATGCAATCATGACTGTC	390
Qy	721	CTCTACCCAGAAATTTGAAAAATGTACAGTGTCACTAAGAAAGAGCGCTGCAACAT	780
Db	391	CTGTACCCAGACTACTGAAAAATGTACAGTGTCACTGAGAAAGCGCGCTGCGC----	445
Qy	781	AACAGAGAACGCGCACTCTCACTCAAGACAGAAAGACTATAAATTTGCTGACGA	840
Db	446	-----AGCAGCCCACTCTCAATACAGACAGGAGCAGTGTAAATTTGCTGCTGCA	498
Qy	841	CATTATATACAGAGATCTTGAAAAATGTATATAGTGTGAGAAAGACTCAATGTCATG	900
Db	499	CATTATATACAGAGATCTTGAAAAATGTATATAGTGTGAGAAAGACTCAATGTCATG	558
Qy	901	CCAGGAGGTGTGTATAGTGTGAGGAGAGAGTTGAGTGTGCGCAACACCTTCTTT	960
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Qy	961	AAACCTTCATGTGTGTCTCTCTACAGATGTGGGGGTCTGCAATATGAGGGCTGACG	1020
Db	619	AAACCTTCATGTGTGTCTCTCTACAGATGTGGGGGTCTGCAACACAGGGGCTGACG	678
Qy	1021	TGCAATGAAACACAGACAGACTCTGAGCAAGAGCTTATTTGAAATTAAGTGGCTCTC	1080
Db	679	TGCAATGAAACACAGACAGACTCTGAGCAAGAGCTTATTTGAAATTAAGTGGCTCTC	738
Qy	1081	TCTCAAGGCCCCAAACAGTAAACATGATTTTGCACATCACTTCTGCGCATGTCATG	1140
Db	739	TCAAGAGCCCCAAACAGTAAACATGATTTTGCACATCACTTCTGCGCATGTCATG	798
Qy	1141	TCTAACTGATTTTACAGCAAGTTCATTTATTTAGAGCTTCCCTCCGACGACACA	1200
Db	799	TCTAACTGATTTTACAGCAAGTTCATTTATTTAGAGCTTCTGCGACGACACA	858
Qy	1201	CTACACAGTGTGAGGAGGAGCAACAGCTGCGCCCAATTAATGATGAAATTAATCAC	1260
Db	859	TTACACAGTGTGAGGAGGAGCAACAGCTGCGCCCAATTAATGATGAAATTAATCAC	918
Qy	1261	ATCTGAGATGCTGCTGACAGAAATTTATGTTTCTCGATGCTGAGATGACTCA	1320
Db	919	ATGCGCGATGCTGCTGACAGAAATTTATCTTTATTAATCAATGTTGAAGATGACTCA	978
Qy	1321	ACAGATGATTTCCATGACATCTGTGACCAAAACAGAGCTGATGAAAGACTGTGACG	1380
Db	979	ACCAATGATTTCCATGATGCTGTGACCAAAACAGAGCTGATGAAAGACTGTGACG	1038
Qy	1381	TGTGTCTGACAGGCGGCTTCCGCTGCGAGCTGTGAGACCCCAAAAGAACTAGACAGA	1440
Db	1039	TGTGTCTGACAGGCGGCTTCCGCTGCGAGCTGTGAGACCCCAAAAGAACTAGATAGA	1098
Qy	1441	AACATGACAGTGTGTCTGTAAACAACTTTCCCAAGCAATGTGGGCGCAACGA	1500
Db	1099	GACTCATGTGATGTGTCTGTAAACAACTTTCCCTAATTCATGTGAGGCAACAGG	1158
Qy	1501	GAAATTTGATGAAACACATGCTGTGTATGTTAAAGAACTGTCCAAAGAAATCAGCCC	1560
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Qy	1561	CTAAATCTGGAAAAATGTGCTGTGATGTACAGAAAGTCCACAGAAATGTTTAA	1620
Db	1219	CTAAATCTGGAAAAATGTGCTGTGATGTACAGAAACACACAGAAATGTTTAA	1278
Qy	1621	GGAAAGATTTCCACACACCAACATCAGCTGTTAACAGCGGCATGTACGAACCGCAG	1680
Db	1279	GGAAAGATTTCCACCATCAACATCAGTGTTAACAGAAACCGTGTGAAATCAGCTG	1338
Qy	1681	AAGCTTTGAGCCAGAGATTTTCAATATGATGAAGAGTGTGTGTGTCTTCAATAT	1740
Db	1339	AAGCATTTGATGTACAGACTGTCTTTAGTGAAGAGTATGCGCTGTGTCCATGTAT	1398
Qy	1741	TGAAAAAGACCAAAATGAGCTAATCTAGAGATCCGTAACCTGCGCAGGCTTT	1793
Db	1399	TGAAAAAGCCACATCTAATCAATGATCAATCAAGTTTCAATGTCACATTTT	1451
RESULT 4			
A0081137			
LOCUS			
DEFINITION			
A0081137 Oncorhynchus mykiss Kidney infected by infectious			
hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KI2,			
mRNA sequence.			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Oncorhynchus mykiss (rainbow trout)			
Oncorhynchus mykiss			
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
REFERENCE			
1 (bases 1 to 1067)			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
CONTACT: Masahiro Sakai			
Faculty of Agriculture			
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan			
Email: m.sakai@cc.miyazaki-u.ac.jp.			
LOCATION/Qualifiers			
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FEATURES			
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infectious hematopoietic necrosis virus"			
/note="common name:rainbow trout ; infected by infectious			
hematopoietic necrosis virus"			
ORIGIN			
Query Match			
Best Local Similarity 98.8%; Pred. No. 3e-261; Length 1067;			
Matches 976; Conservative 0; Mismatches 10; Indels 2; Gaps 2;			
Qy	2706	CTAGACGTATCATGCTGATGCTGTTCTGTGTAATGTTATCCGCTCAATTC	2765
Db	82	CTTGGGATATATATGATGCTGTTCTGTGTAAATGTTATCCGCTCAATTC	141
Qy	2766	ACACAAATATGAGCGGAGGAGCATTAAGTAAAGCTGGGTGCTAATGATGAGCTA	2825
Db	142	ACACAAATATGAGCGGAGGAGCATTAAGTAAAGCTGGGTGCTAATGATGAGCTA	201
Qy	2826	ACTCAATTAATTTGGGTGCTCACTGCGCTTTTCAAGTGGGAAACCTGTGCGGCA	2885
Db	202	ACTCAATTAATTTGGGTGCTCACTGCGCTTTTCAAGTGGGAAACCTGTGCGGCA	261
Qy	2886	GCTCATTAATGATGCGCAACGCGCGGAGAGCGGTTTGCTATTGGGCGCTTTC	2945

Db	262	GCTGCATTATGATATGGCCAAACGCGGAGAGAGCGGTTTGCGATTGAGCGCTTTC	321
QY	2946	CGCTTCCTGCTCACTGACTCGCTGCGCTCGGTCGTTCGAGTCGCGGCGAGCGGTATCAGC	3005
Db	322	CGCTTCCTGCTCACTGACTCGCTGCGCTCGGTCGTTCGAGTCGCGGCGAGCGGTATCAGC	381
QY	3006	TCACTCAAAAGCGCGTATATACGGTTATCCAAGATCAGGAGGATTAACGACGAAAGAACAT	3065
Db	382	TCACTCAAAAGCGCGTATATACGGTTATCCAAGATCAGGAGGATTAACGACGAAAGAACAT	441
QY	3066	GTGAGCAAAAGCCGACGCAAAAGCCGAGAAACCGTAAAGAGCCGCGTTCGTGCGCTTTT	3125
Db	442	GTGAGCAAAAGCCGACGCAAAAGCCGAGAAACCGTAAAGAGCCGCGTTCGTGCGCTTTT	501
QY	3126	CCATAGGCTCCGCCCCCTGACGAGCATACAAAAAATGACGCTCAAGTCAGAGGTGAGCG	3185
Db	502	CCATAGGCTCCGCCCCCTGACGAGCATACAAAAAATGACGCTCAAGTCAGAGGTGAGCG	561
QY	3186	AAACCCGACAGGACTATTAAGATACAGGCGTTTCCCTGAGAGCTCCCTGTCGCGCTC	3245
Db	562	AAACCCGACAGGACTATTAAGATACAGGCGTTTCCCTGAGAGCTCCCTGTCGCGCTC	621
QY	3246	TCCTGTCCGACCCCTGCGGCTTACCAGGATCCTGTTCGCTTTCCTTCCTTCGGGAAAGGT	3305
Db	622	TCCTGTCCGACCCCTGCGGCTTACCAGGATCCTGTTCGCTTTCCTTCCTTCGGGAAAGGT	681
QY	3306	GGCGCTTTCCTCAATAGCTCAGCGCTGATAGGATCTCAAGTTCGAGGTAGGTGTTGCGTCCAA	3365
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QY	3366	GCTGAGGCTGTGTGCAAGAACCCCGGTTCAAGCCGACGAGCGTGCAGCTTATCCGATACCTA	3425
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QY	3426	TGCTCTTAGATCCAAACCCGCTTAAGACACGACTTATGCGCACTGCGACGACCACTGTGTA	3485
Db	802	TGCTCTTAGATCCAAACCCGCTTAAGACACGACTTATGCGCACTGCGACGACCACTGTGTA	861
QY	3486	CAGATTTAGCAGAGGAGGTATGTAGGGGGGTCTACAGAGTCTTGAAGTGTGTGCCCTTA	3545
Db	862	CAGATTTAGCAGAGGAGGTATGTAGGGGGGTCTACAGAGTCTTGAAGTGTGTGCCCTTA	921
QY	3546	CTACGGCTACCTAAGAAACAGTATTTGTGTATCGCGCTCTGCTGAAGCCAGTTACCTT	3605
Db	922	CTACGGCTACCTAAGAAACAGTATTTGTGTATCGCGCTCTGCTGAAGCCAGTTACCTT	981
QY	3606	CGAAAAAAGAGTTGGTAGCTTTGATCCGCAACAAACACACGCTGTGTAGCGGTGTTT	3665
Db	982	CGAAAAAAGAGTTGGTAGCTTTGATCCGCAACAAACACACGCTGTGTAGCGGTGTTT	1040
QY	3666	TTTTGTTCGACAGCAGCATTAACCGCG 3693	
Db	1041	TTTTGTTCGCGAGCATTAACCGCG 1067	

RESULT 5					
LOCUS	CK283361/c				
DEFINITION	CK283361	954 bp	mRNA	linear	EST 02-AUG-2004
ACCESSION	ESF746083	Nicotiana benthamiana mixed tissue cDNA library,			
KEYWORDS	normalized, full-length Nicotiana benthamiana cDNA clone NIBAGS0 5'				
VERSION	CK283361				
SOURCE	CK283361.1	GI:39855898			
ORGANISM	EST.				
REFERENCE	Nicotiana benthamiana				
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Nicotiana.				
	1 (bases 1 to 954)				
	Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,				
	Staskawicz, B., Jin, H. and Baker, B.				

FEATURES	source
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ORIGIN	
Query Match	17.8%; Score 939.4; DB 7; Length 954;
Best Local Similarity	99.9%; Freq. No. 8.9e-259;
Matches 940; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
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894 CTTTCATGAAAGCGCGCGTGAATTCGAAATCTCGTATGCGACGTTGGCGTCTTGG 835	
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834 TCGGTCATTTGAAACCCCAAGTCCCGCTCGAAGAACTCGTCAAGAAAGCGATGAAAG 775	
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774 CGATGCGCTGGGAATCGGGAAGCGCGGATACCGTAAAGACGAGAAGCGGTCAAGCCATT 715	
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714 CGCGCCCAAGCTCTTCAGCATATACAGGGTAGCAACGCTATGCTTCGATAGCGGTCCG 655	
Db	4291 CCAACACCAAGCGCGGCACAGTCGATGATTCAGAAAAGCGGCATTTTCCACATGATAT 4350
Qy	
654 CCAACACCAAGCGCGGCACAGTCGATGATTCAGAAAAGCGGCATTTTCCACATGATAT 595	
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Qy	
594 TCGGCAAGACAGGATTCGCAATGGGTCAACGACGATCTCGCGCGTCCGGGACATGGCGCCCT 535	
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534 TGAAGCTGGCAACGATTCGGCTGGCGCGAGCCCTGATGCTCTTCGTCAGATCATCTCT 475	
Db	4471 GATGACAAAGACCGGCTTCATCCGATACGTGCTCGCTCGATGCGATGTTGGCTTGGT 4530
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474 GATGACAAAGACCGGCTTCATCCGATACGTGCTCGCTCGATGCGATGTTGGCTTGGT 415	

QY 4531 GGTGGAATGGGACAGTAGCCGGATCAACGGTATGACAGCCCGGCAATTGCATCAGCCATGA 4530
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QY 4591 TGGATACCTTCTCGGACAGGACAGTAGATGACAGAGATCTGCCCCGGCACTTCG 4650
Db 354 TGGATACCTTCTCGGACAGGACAGTAGATGACAGAGATCTGCCCCGGCACTTCG 295
QY 4651 CCATATACAGCCAGTCCCTTCCGCTTCAGTGAACAAGTGAAGCAGTGCAGCAAGAA 4710
Db 294 CCATATACAGCCAGTCCCTTCCGCTTCAGTGAACAAGTGAAGCAGTGCAGCAAGAA 235
QY 4711 CGCCGCTGTCGACAGCAGATAGCGCGCTGCTGCTGATGATTCATTCAGGCGAC 4770
Db 234 CGCCGCTGTCGACAGCAGATAGCGCGCTGCTGCTGATGATTCATTCAGGCGAC 175
QY 4771 CGGACAGGTGCTTGTGACAAAAAGAACCGGCGCCCTGCGTGAAGCCGGAACAG 4830
Db 174 CGGACAGGTGCTTGTGACAAAAAGAACCGGCGCCCTGCGTGAAGCCGGAACAG 115
QY 4831 CGGATCAGAGCCGATGCTGTTGTGCTGCTGATGATGCGGATGACCTTCCACC 4890
Db 114 CGGATCAGAGCCGATGCTGTTGTGCTGCTGATGATGCGGATGACCTTCCACC 55
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RESULT 6
LOCUS CK298208/c
DEFINITION 947 bp mRNA linear EST 02-AUG-2004
EST760922 Nicotiana benthamiana mixed tissue cDNA library, NBMDE30 5' end, mRNA sequence.

ACCESSION CK298208
VERSION CK298208
KEYWORDS
SOURCE
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Nicotiana.

REFERENCE
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karanicheva, S.A., Day, B., Staskiewicz, B., Jin, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST760923
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1..947

FEATURES
Source
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/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMDE30"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DHIOB-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (Pseudomonas syringae pv tomatos 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 17.5%; Score 924.6; DB 7; Length 947;
Best local similarity 99.6%; Pred. No. 1.7e-254;
Matches 927; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4001 GCTGGAAGATCATCCAGCCGCGCTCCCGAAAAACGATTCGAGGCCCACTTCTATAGA 4060
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QY 4061 AGCGCGCGGTGAATGAAATCTCGTGAATGCGAGTGGGCGCGCTGCTGCGTCAATT 4120
Db 887 AGCGCGCGGTGAATGAAATCTCGTGAATGCGAGTGGGCGCGCTGCTGCGTCAATT 828
QY 4121 CGAATCCCAAGTCCCGCTCAGAAAGACTGTCAGAAAGCGATAGAGCGATGCGCTG 4180
Db 827 CGAATCCCAAGTCCCGCTCAGAAAGACTGTCAGAAAGCGATAGAGCGATGCGCTG 768
QY 4181 CGAATCGGAGAGGCGGATACCGTAAGCAAGAGAAAGCGGTAGCCCATTCGCGCGAAG 4240
Db 767 CGAATCGGAGAGGCGGATACCGTAAGCAAGAGAAAGCGGTAGCCCATTCGCGCGAAG 708
QY 4241 CTCTTCAGCAATATACAGGGGTAGCCAAAGCTATGCTGATAGCGGTCCGCAACCCAG 4300
Db 707 CTCTTCAGCAATATACAGGGGTAGCCAAAGCTATGCTGATAGCGGTCCGCAACCCAG 648
QY 4301 CCGGCCACAGTGAATGAATCCAGAAAGCGCCATTTTCACCATGATATTTGGCAGCA 4360
Db 647 CCGGCCACAGTGAATGAATCCAGAAAGCGCCATTTTCACCATGATATTTGGCAGCA 588
QY 4361 GGCATCGCCATGATGACAGAGAGATCTCGCGCTCGGCGCATGCGCGCTTGAAGCTGGC 4420
Db 587 GGCATCGCCATGATGATGACAGAGAGATCTCGCGCTCGGCGCATGCGCGCTTGAAGCTGGC 528
QY 4421 GAAACAGTTGCGGTGGCGCAGAGCCCTGATGCTCTTGTGATGATGATCTGATGCAAG 4480
Db 527 GAAACAGTTGCGGTGGCGCAGAGCCCTGATGCTCTTGTGATGATGATCTGATGCAAG 468
QY 4481 ACCGCGTTCCATCCAGATACGTCGCTGCTGATGATGATGATGATGATGATGATG 4540
Db 467 ACCGCGTTCCATCCAGATACGTCGCTGCTGATGATGATGATGATGATGATGATG 408
QY 4541 GCAGGTAGCCGATCAAGCGATGACAGCGCGCGCATTTGATGATGATGATGATGATG 4600
Db 407 GCAGGTAGCCGATCAAGCGATGACAGCGCGCGCATTTGATGATGATGATGATGATG 348
QY 4601 CTCGGCAGAGCAGAGTAGATGACAGAGATCTGCCCCGCACTTGGCCCAATAGCAG 4660
Db 347 CTCGGCAGAGCAGAGTAGATGACAGAGATCTGCCCCGCACTTGGCCCAATAGCAG 288
QY 4661 CCAGTCCCTTCCCGCTTGAATGACAGCGTGAAGCAGAGTGGGAGAAAGCCCGTGGT 4720
Db 287 CCAGTCCCTTCCCGCTTGAATGACAGCGTGAAGCAGAGTGGGAGAAAGCCCGTGGT 228
QY 4721 GGCACAGCAGATAGCCGCGCTGCTGCTGCTGATTCATTCAGAGGACCGGACAGGTC 4780
Db 227 GGCACAGCAGATAGCCGCGCTGCTGCTGCTGATTCATTCAGAGGACCGGACAGGTC 168
QY 4781 GGTCTTGAACAAAAAGAACCGGCGCGCTTGGCTGACAGCGCGGAAACAGCGCGCATCAGA 4840
Db 167 GGTCTTGAACAAAAAGAACCGGCGCGCTTGGCTGACAGCGCGGAAACAGCGCGCATCAGA 108
QY 4841 GAGCGCAATGCTGTTGGCCAGTCAATAGCCGAATGAGCTCTTCCACCAAGCGCGCGG 4900
Db 107 GAGCGCAATGCTGTTGGCCAGTCAATAGCCGAATGAGCTCTTCCACCAAGCGCGCGG 48
QY 4901 AGAACCTGCTGCAATTCATCTTGTCAATC 4931

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Db 47 AGAAGCTGCGTGCATCCATCTTGTTCATC 17
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RESULT 7 1089 bp mRNA linear EST 30-JUL-2002
AU081124 Oncorhynchus mykiss Kidney infected by infectious
LOCUS AU081124 Oncorhynchus mykiss Kidney infected by infectious
DEFINITION hematopoietic necrosis virus Oncorhynchus mykiss CDNA clone KG.12,
mRNA sequence.
ACCESSION AU081124
VERSION AU081124.1 GI:6431472
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1089)
AUTHORS Kono,T., Sakai,M. and Lapetra,S.E.
TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT Contact: Masahito Sakai
Faculty of Agriculture
Miyazaki University
1-1-nishi gakuenibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
Location/Qualifiers
1. 1089
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="KG.12"
/issue_type="Kidney"
/clone_lib="Oncorhynchus mykiss Kidney infected by
infectious hematopoietic necrosis virus"
/note="common name:rainbow trout ; infected by infectious
hematopoietic necrosis virus"
ORIGIN
Query Match 17.4%; Score 919.8; DB 1; Length 1089;
Best Local Similarity 97.2%; Pred. No. 4.2e-253;
Matches 979; Conservative 0; Mismatches 22; Indels 6; Gaps 4;
QY 2706 CTGACGCTATCATGTCATAGCTGTTCTCTGTGTGAATTTGTTATCCGCTCACAAATTC 2765
DB 83 CTGGCGCTAATCATGTCATAGCTGTTCTCTGTGTGAATTTGTTATCCGCTCACAAATTC 142
QY 2766 ACACAATATCGAGCGGAGCATTAAGTGTAAAGCCCTGGGGTGCCTTAATGATGAGCTA 2825
DB 143 ACACAAATATCGAGCGGAGCATTAAGTGTAAAGCCCTGGGGTGCCTTAATGATGAGCTA 202
QY 2826 ACTCACATTAATTCGTTGGCTCACTGCGCTTTCCAGTCGGGAAACCTGTGTCGA 2885
DB 203 ACTCACATTAATTCGTTGGCTCACTGCGCTTTCCAGTCGGGAAACCTGTGTCGA 262
QY 2886 GCTGCATTAATGAATCGGCCAACCGCGGGAGAGCGGTTTGGTATTTGGGCGCTCTTC 2945
DB 263 GCTGCATTAATGAATCGGCCAACCGCGGGAGAGCGGTTTGGTATTTGGGCGCTCTTC 322
QY 2946 CGCTTCCTCGCTCATGCTCGCGCGCTCGTTCGCTGGGAGAGCGGTATTCAGC 3005
DB 323 CGCTTCCTCGCTCATGCTCGCGCTCGTTCGCTGGGAGAGCGGTATTCAGC 382
QY 3006 TCACTCAAAGCGGTAAATACGGTTATCCACAGATTCAGGGGATTAACGACGAGAAACAT 3065
DB 383 TCACTCAAAGCGGTAAATACGGTTATCCACAGATTCAGGGGATTAACGACGAGAAACAT 442
QY 3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAGGCGCGTTGCTGCGGTTTTT 3125
DB 443 GTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAGGCGCGTTGCTGCGGTTTTT 502

QY 3126 CCATAGGCTCGGCCCCCTGACGAGCATCAAAAAATGACGCTCAAGTCAGAGGTGCG 3185
DB 503 CCATAGGCTCGGCCCCCTGACGAGCATCAAAAAATGACGCTCAAGTCAGAGGTGCG 562
QY 3186 AAACCCGACAGACTATTAAGATACAGGCGCTTTCCTCGGAAAGCTCCTCGTGCCTC 3245
DB 563 AAACCCGACAGACTATTAAGATACAGGCGCTTTCCTCGGAAAGCTCCTCGTGCCTC 622
QY 3246 TCTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCTTTCTCCTTCGGGAAGCGT 3305
DB 623 TCTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCTTTCTCCTTCGGGAAGCGT 682
QY 3306 GAGCGTTTCATATAGCTCAGCGTATGAGGTATCTAGTTCGGGTATGAGTTCGCTCAA 3365
DB 683 GAGCGTTTCATATAGCTCAGCGTATGAGGTATCTAGTTCGGGTATGAGTTCGCTCAA 742
QY 3366 GCTGGGCTGTGTGACGAAACCCCGTTCAAGCCGACCGCTGCGCTTATCCGGTAACTA 3425
DB 743 GCTGGGCTGTGTGACGAAACCCCGTTCAAGCCGACCGCTGCGCTTATCCGGTAACTA 802
QY 3426 TCGTCTTGAGTCCAAACCGGTAAACACGACTTATCCCACTGACGACGCACTGTAA 3485
DB 803 TCGTCTTGAGTCCAAACCGGTAAACACGACTTATCCCACTGACGACGCACTGTAA 862
QY 3486 CAGGATTAACGACGCGAGTATGTAGGCGGTCTACAGAGTTCTGAAAG-TGTGGCCTTA 3544
DB 863 CAGGATTAACGACGCGAGTATGTAGGCGGTCTACAGAGTTCTGAAAGTTGTGGCCTTA 922
QY 3545 ACTACGCTACACTAGAAAGAACATATTTGATCTGCGCTGCTGTAAGCCAGTAACT 3604
DB 923 ACTACGCTACACTAGAAAGAACATATTTGATCTGCGCTGCTGTAAGCCAGTAACT 982
QY 3605 TCGGAAAAAGAGTGTGAGCTCTT-GATTCGGCAAAACCA---CCGCTGTAGCGGT 3660
DB 983 TCGGAAAAAGAGTGTGAGCTCTTGTGATTCGGCAAAACCAACCCGTGGGAAAGGGGG 1042
QY 3661 GGTTTTTTTGTTGTCAGCA-GCAGATTAACCGCGAGAAAAAAGAT 3706
DB 1043 TGTCTTTTGTGTGCAAGCAGCAGATTAACCGCGAAAAAAGCGAT 1089
RESULT 8
CK284786/c 935 bp mRNA linear EST 02-AUG-2004
LOCUS CK284786
DEFINITION EST747508 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBWAQ41.5',
end, mRNA sequence.
ACCESSION CK284786
VERSION CK284786.1 GI:39858698
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 935)
AUTHORS Buell,C.R., Hart,A., Zismann,V., Karanymcheva,S.A., Day,B.,
Skaskawicz,B., Jin,H. and Baker,B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: EST747509
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
SOURCE Location/Qualifiers
1. 935
/organism="Nicotiana benthamiana"
/mol_type="mRNA"

/db xref="taxon:4100"
 /clone="NBMAQ41"
 /tissue_type="abiotic and biotic stress-treated leaves,
 callus tissue and root tissue"
 /lab_host="DH10B-Tona"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA
 library, normalized, full-length"
 /note="Vector: PCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: RNA was isolated from Nicotiana benthamiana
 tissues that include callus, roots from liquid culture
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
 cold-stressed leaves (5 C, 3 hr, 6hr), and pathogen
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;
 Xanthomonas campestris pv campestris 12 hr, 18hr;
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
 campestris pv vesicatoria 18hr). RNA was isolated from
 these tissues and pooled in approximately equal molar
 amounts."

ORIGIN

Query Match 17.4%; Score 918.6; DB 7; Length 935;

Best Local Similarity 99.6%; Pred. No. 8.9e-253;

Matches 921; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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OY 4030 AAAACGATTCGAAAGCCCACTTTTCATAGAAAGCGCGGTGGAATGGAATCTCGTAT 4089
DB 935 AAAACGATTCGAAAGCCCACTTTTCATAGAAAGCGCGGTGGAATGGAATCTCGTAT 876
OY 4090 GGCAGGTTGGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4149
DB 875 GGCAGGTTGGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816
OY 4150 CGTCAAGAGGCGATAGAAAGCGATGCGCTCGAATGCGGCGGCGATACCGTAAAGCA 4209
DB 815 CGTCAAGAGGCGATAGAAAGCGATGCGCTCGAATGCGGCGGCGATACCGTAAAGCA 756
OY 4210 CGAAGAACGGTTCGCGCCATTCGCGCAAGCTCTTCAAGCAATTCACGGGTAGCCAAAG 4269
DB 755 CGAAGAACGGTTCGCGCCATTCGCGCAAGCTCTTCAAGCAATTCACGGGTAGCCAAAG 696
OY 4270 CTATGCTCTGATAGCGGCTCGGCAACACCGCGGCAAGTCGATGATGATCAGAAAAAGC 4329
DB 695 CTATGCTCTGATAGCGGCTCGGCAACACCGCGGCAAGTCGATGATGATCAGAAAAAGC 636
OY 4330 GGCATTTTCCATGATATTTCCGCAAGCGGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 4389
DB 635 GGCATTTTCCATGATATTTCCGCAAGCGGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 576
OY 4390 GCGCGTGGGCGATGCGGCGCTTGAAGCTGCGCAAGTCGCTGCGCGCGGCGGCGCTGAT 4449
DB 575 GCGCGTGGGCGATGCGGCGCTTGAAGCTGCGCAAGTCGCTGCGCGCGGCGGCGCTGAT 516
OY 4450 GCTCTTCTGCGATGATCTGATGCAAGACCGGCTTCCATCCGATGATGCTGCTGCTGCT 4509
DB 515 GCTCTTCTGCGATGATCTGATGCAAGACCGGCTTCCATCCGATGATGCTGCTGCTGCT 456
OY 4510 CGATGGAATGTTTCCGTTGGTGTGGAATGGGCAAGTACCGGATCAAGCGTATGCAACC 4569
DB 455 CGATGGAATGTTTCCGTTGGTGTGGAATGGGCAAGTACCGGATCAAGCGTATGCAACC 396
OY 4570 GCGCGATTCGATCAGCCATGATGATCTTTCTCGGCAAGACAGTGAATGACAGGA 4629
DB 395 GCGCGATTCGATCAGCCATGATGATCTTTCTCGGCAAGACAGTGAATGACAGGA 336
OY 4630 GATCTGCGCGCGCATTTGCGCCATAGAGCAAGTCCTTCCGCTTCAAGTGAACAAGT 4689
DB 335 GATCTGCGCGCGCATTTGCGCCATAGAGCAAGTCCTTCCGCTTCAAGTGAACAAGT 276
OY 4690 CGAGCAGAGTGGCAAGAAAGCGCGCTGCTGCGGCAAGCAAGTACCGGCTGCTGCTGCT 4749
DB 275 CGAGCAGAGTGGCAAGAAAGCGCGCTGCTGCGGCAAGCAAGTACCGGCTGCTGCTGCT 216
OY 4750 CTTGACGTTTCATTCAGGCGCACCGGACAGGTCGCTTTCGACAAAAGAACCGGCGCCCT 4809

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DB 215 CTTGACGTTTCATTCAGGCGCACCGGACAGTTCGCTTTCGACAAAAGAACCGGCGCCCT 156
OY 4810 GCGCTGACAGCGCGGAACAACGCGCGCATCAGACAGCGGATTTCTGTTGGCCAGTCAT 4869
DB 155 GCGCTGACAGCGCGGAACAACGCGCGCATCAGACAGCGGATTTCTGTTGGCCAGTCAT 96
OY 4870 AGCGGAATAGCTCTCCACCCCAAGCGCGGGAAGAACTCGGTGCAATCTGTTCAA 4929
DB 95 AGCGGAATAGCTCTCCACCCCAAGCGCGGGAAGAACTCGGTGCAATCTGTTCAA 36
OY 4930 TCATCGAAAGCATTCATCCGCT 4954
DB 35 TCATCGAAAGCATTCATCCGCT 11

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RESULT 9

CK256977/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@igf.org
 Clones can be requested from the University of Arizona Genomics
 Institute via http://genome.arizona.edu/orders/
 Seq primer: APT TAG GTG ACA CTA TAG.

FEATURES

Source

1..936
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="POCD170"
 /tissue_type="callus"
 /lab_host="DH10B-Tona"
 /clone_lib="potato callus cDNA library, normalized and
 full-length"
 /note="Vector: PCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: RNA was isolated from Solanum tuberosum var.
 Kennebec callus tissue grown on solid media."

ORIGIN

Query Match 17.2%; Score 911; DB 7; Length 935;

Best Local Similarity 99.9%; Pred. No. 1.4e-250;

Matches 922; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OY 4010 TCATCCAGCGCGGCTCCC-GGAAACGATTCGAAAGCCCACTTTTCATAGAAAGCGGCG 4068
DB 936 TCATCCAGCGCGGCTCCC-GGAAACGATTCGAAAGCCCACTTTTCATAGAAAGCGGCG 877
OY 4069 GTGAATCGAAATCTCGTATGCGAGTGGCGTGGCTTGTGCTGCTGCTGCTGCTGCTGCT 4128
DB 876 GTGAATCGAAATCTCGTATGCGAGTGGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 817
OY 4129 AGAGTCCCGCTCAGAAAGAACTCTGTCAGAAAGGCGATGAAAGGCGATGCGTGAATCG 4188
DB 816 AGAGTCCCGCTCAGAAAGAACTCTGTCAGAAAGGCGATGAAAGGCGATGCGTGAATCG 757
OY 4189 GAGGCGGATACGTTAAAGACAGAGAAAGCGGTACGCCCATTCGCGCCAAAGCTTTAG 4248

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Db      756 GAGCGGCATACCCGTAAGACAGAGAAAGCGCTCAGCCCATTCGCGCAAGCTCTTCAAG 697
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Db      696 CAATATCAAGGGTAGCCAAAGCTATGCTCTGATAGAGGTCGCGCAACCCAGCGCGCAC 637
Qy      4309 AGTCGATGAATTCAGAAAAAGCGCCATTTTCCACCATGATATTCCGCAAGAGGAGCATCGC 4368
Db      636 AGTCGATGAATTCAGAAAAAGCGCCATTTTCCACCATGATATTCCGCAAGAGGAGCATCGC 577
Qy      4369 CATGGGTACACACAGATGCTTCGCGGTGGGATGCGCGCTTGAGCCTGGCGAAACAGTT 4428
Db      576 CATGGGTACACACAGATGCTTCGCGGTGGGATGCGCGCTTGAGCCTGGCGAAACAGTT 517
Qy      4429 CGGCTGGGCGAGCGCCCGATGCTCTTGTCCAGATCACTCTGATTCGCAAGACCGGCTT 4488
Db      516 CGGCTGGGCGAGCGCCCGATGCTCTTGTCCAGATCACTCTGATTCGCAAGACCGGCTT 457
Qy      4489 CCATCCGATACGTCCTGCTCGATGCGATGTTTTCGTTGGTGGTCAATGGGCGAGTAG 4548
Db      456 CCATCCGATACGTCCTGCTCGATGCGATGTTTTCGTTGGTGGTCAATGGGCGAGTAG 397
Qy      4549 CCGGATCAAGCGGTATGACGCGCGCGCATTTGCATACAGCCATGATGATATCTTTTCGCGAG 4608
Db      396 CCGGATCAAGCGGTATGACGCGCGCGCATTTGCATACAGCCATGATGATATCTTTTCGCGAG 337
Qy      4609 GAGCAAGGTGAGTACAGAGAGATCTTCGCGCGCGCATTTCCGCAATGACAGCCAGTCCC 4668
Db      336 GAGCAAGGTGAGTACAGAGAGATCTTCGCGCGCGCATTTCCGCAATGACAGCCAGTCCC 277
Qy      4669 TTCCCGCTTCAAGTACACAGTGCAGACAGCTGCGCAAGAAAGCGCGTCTGTCGCAAGC 4728
Db      276 TTCCCGCTTCAAGTACACAGTGCAGACAGCTGCGCAAGAAAGCGCGTCTGTCGCAAGC 217
Qy      4729 ACGATAGCCGCGCTGCTCTGCTGCAAGTTCAATTCAGGGCACCGGACAGTCTTTGA 4788
Db      216 ACGATAGCCGCGCTGCTCTGCTGCAAGTTCAATTCAGGGCACCGGACAGTCTTTGA 157
Qy      4789 CAAAAAAGACCGGGCGCGCCCTGCGCTGACAGCGCGGAAACAGCGCGGATCAAGAGACCGGA 4848
Db      156 CAAAAAAGACCGGGCGCGCCCTGCGCTGACAGCGCGGAAACAGCGCGGATCAAGAGACCGGA 97
Qy      4849 TTGCTGTGTGAGCCAGTATAGCCGAATAGCTCTCCACCCAGCGCGCGGAGAACCTG 4908
Db      96 TTGCTGTGTGAGCCAGTATAGCCGAATAGCTCTCTCCACCCAGCGCGCGGAGAACCTG 37
Qy      4909 CGTGCATTCATCTTTGTTCAATC 4931
Db      36 CGTGCATTCATCTTTGTTCAATC 14

RESULT 10
LOCUS   CK287930/c
DEFINITION
EST750652 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NMBCT5 5'
end, mRNA sequence.
ACCESSION
CK287930
VERSION
CK287930.1 GI:39864940
KEYWORDS
EST.
SOURCE
Nicotiana benthamiana
ORGANISM
Nicotiana benthamiana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 910)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskiewicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
OTHER ESTs: EST750653
COMMENT
Contact: Robin Buell

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1..910
/organism="Nicotiana benthamiana"
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/db_xref="taxon:4100"
/clone="NMBCT5"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TorA"
/clone_id="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture,
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 17.2%; Score 907; DB 7; Length 910;
Best Local Similarity 100.0%; Pred. No. 2e-249;
Matches 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4025 CCGGAAAACGATTCGGAAGCCCACTTTATAGAAAGCGCGGTGAAATCGAAATCTC 4084
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Qy      4085 GTATGCGCAGTTGGGGTGGCTTGTGTCGTCATTTGAAACCCAGAGTCCCGTCGAA 4144
Db      850 GTATGCGCAGTTGGGGTGGCTTGTGTCGTCATTTGAAACCCAGAGTCCCGTCGAA 791
Qy      4145 GAACTCGTCAAGAAAGGATAGAAAGCGATGCGCTGCAATCCGGAGACGGGATACGCTA 4204
Db      790 GAACTCGTCAAGAAAGGATAGAAAGCGATGCGCTGCAATCCGGAGACGGGATACGCTA 731
Qy      4205 AAGCAGGAGAAAGCGGTACAGCCATTGCGCGCAAGCTCTTCAGCAATATCACGGGTAGC 4264
Db      730 AAGCAGGAGAAAGCGGTACAGCCATTGCGCGCAAGCTCTTCAGCAATATCACGGGTAGC 671
Qy      4265 CAAGCTATGTCTGATAGCGGTCCGCGACACCAAGCGCGGACAGTGCATGAATCCAGA 4324
Db      670 CAAGCTATGTCTGATAGCGGTCCGCGACACCAAGCGCGGACAGTGCATGAATCCAGA 611
Qy      4325 AAAGCGGCATTTTCCACCATGATATTCCGCAAGAGGAGCATTCGCANTGGGTCAAGAGAG 4384
Db      610 AAAGCGGCATTTTCCACCATGATATTCCGCAAGAGGAGCATTCGCANTGGGTCAAGAGAG 551
Qy      4385 ATCTCGCGCTCGGGGATGCGCGCTTGAGCCTGCGGCAAGATTTGCGCTGCGCGAGCCC 4444
Db      550 ATCTCGCGCTCGGGGATGCGCGCTTGAGCCTGCGGCAAGATTTGCGCTGCGCGAGCCC 491
Qy      4445 CTGATGCTCTTGTCCAGATCATCTGATGAGCAAGACCGGCTTCCATCCGATGAGTGC 4504
Db      490 CTGATGCTCTTGTCCAGATCATCTGATGAGCAAGACCGGCTTCCATCCGATGAGTGC 431
Qy      4505 TCGCTGATGAGATGTTTGGCTTGTGTCGATGAGGAGGTAGCCGGATCAAGCGGTAG 4564
Db      430 TCGCTGATGAGATGTTTGGCTTGTGTCGATGAGGAGGTAGCCGGATCAAGCGGTAG 371
Qy      4565 CAGCGCGCGCATTCAGCAAGCCATGATGATATCTTTCTCGGCAAGCAAGGTGAGATGA 4624
Db      370 CAGCGCGCGCATTCAGCAAGCCATGATGATATCTTTCTCGGCAAGCAAGGTGAGATGA 311

```

The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ART TAG GTG ACA CTA TAG.

Location/Qualifiers

QY	4825	CAGGAGATTCCTGGCCCGGACATTGGCCCAATGAGCAGCGCTTCGCCGTTAGTAGAC	4864
Db	310	CAGGAGATCTGCGCCCGGACCTTGCCCAATGAGCAGCGCTTCGCCGTTAGTAGAC	251
QY	4685	AACGTGAGGACAGCTGTGGCAAGGACGCCGTGTGTGGCAGCCACGATAGCCGCGCTGC	4744
Db	250	AACCTGAGGACAGCTGTGGCAAGGACGCCGTGTGTGGCAGCCACGATAGCCGCGCTGC	191
QY	4745	CTGTGCTCGAGTTTCATTACAGGGACCGGACAGGTGCGTCTTGACAAATAAAGACCGGCGC	4804
Db	190	CTGTGCTCGAGTTTCATTACAGGGACCGGACAGGTGCGTCTTGACAAATAAAGACCGGCGC	131
QY	4805	CCCTGCGCTGACAGCCGGAAACAAGCGCGCATCAGAGCAGCCGATTTGTTGTGCCCA	4864
Db	130	CCCTGCGCTGACAGCCGGAAACAAGCGCGCATCAGAGCAGCCGATTTGTTGTGCCCA	71
QY	4865	GTCATAGCGGAATAGCTCTCCACCAGCGCGGAGAACCTGTGTCATTCATCTTG	4924
Db	70	GTCATAGCGGAATAGCTCTCCACCAGCGCGGAGAACCTGTGTCATTCATCTTG	11
QY	4925	TTCAATC	4931
Db	10	TTCAATC	4

RESULT 11	
LOCUS	CL021189
DEFINITION	CL021189 1049 bp DNA linear GSS 31-DEC-2003
ACCESSION	CH216-8A14_RM1.1 CH216 <i>Xenopus tropicalis</i> genomic clone CH216-8A14, genomic survey sequence.
VERSION	CL021189.1 GI:40463002

SOURCE ORGANISM	ORGANISM
Xenopus tropicalis (western clawed frog)	Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE	AUTHORS
1 (bases 1 to 1049)	Kremtitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

TITLE	A physical map of the xenopus tropicalis genome
JOURNAL	Unpublished (2003)
COMMENT	Contact: Richard K Wilson

Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu

Insert Length: 175000 Std Error: 0
Seq primer: RML TAGACTCACTATAGGAGAGA
Class: BAC ends

High quality sequence start: 43	1040
High quality sequence stop: 888	
Location/Qualifiers	

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    /strain="NH4cristan frog"

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/clone="CH216-8A14"
/sex="male"

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/note="Vector: rTARBAC2.1: CHOBT-216 X

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BAC Library"

ORIGIN

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Matches 929; Conservative	0;	Mismatches 16;	Indels 2;	Gaps 2;

2701 GCTGCTAGACGTAATCATGGTCATAGCTGTTCTCTGTGGAATTGTATCCGCTACA 2760

Db	102	GCAAGCTTGGCGTAAATCATGTCACTACGCTGTTTCCTGTGTGAATATGTATCCGCTACA	161
QY	2761	ATTCCACAACAACATACGAGCCGGAAAGCATAAAGTAAAGCCTGGGGTGCCTAATGAGTG	2820
Db	162	ATTCCACAACAACATACGAGCCGGAAAGCATAAAGTAAAGCCTGGGGTGCCTAATGAGTG	221
QY	2821	AGCTAACTCACTTAATTGGCTTGCCTCACTGGCCGCTTCCAGTGGGAAACCTGTGCG	2880
Db	222	AGCTAACTCACTTAATTGGCTTGCCTCACTGGCCGCTTCCAGTGGGAAACCTGTGCG	281
QY	2881	TGCCAGCTGCATTAATGATCGGCGCAACCGCGGGAGAGAGCGGTATTGCGTATTTGGCGCGC	2940
Db	282	TGCCAGCTGCATTAATGATCGGCGCAACCGCGGGAGAGAGCGGTATTGCGTATTTGGCGCGC	341
QY	2941	TCTTCCGCTTCTCGCTCACTGACTCGCTGCGTCCGTCGTTTCGGCTCGCGGACGCGTA	3000
Db	342	TCTTCCGCTTCTCGCTCACTGACTCGCTGCGTCCGTCGTTTCGGCTCGCGGACGCGTA	401
QY	3001	TCAGCTCACTCAAAAGCGGTAATACGGTATATCCACAAATTCAGGGGATTAACGACGGAAG	3060
Db	402	TCAGCTCACTCAAAAGCGGTAATACGGTATATCCACAAATTCAGGGGATTAACGACGGAAG	461
QY	3061	AAACATGTAGCAAAAGGCACGCAAAAGGCCAGGAACGTTAAAAAAGCGCGGTTGCTGGCG	3120
Db	462	AAACATGTAGCAAAAGGCACGCAAAAGGCCAGGAACGTTAAAAAAGCGCGGTTGCTGGCG	521

[illegible]

DB 522 TTTTTCATATGGCTTCGCCCCCTTGACAGCATCACAAAAATGACAGTCTCTGAGAG 352

QY 3181 TGGCGAAACCCGACAGACTATAAGATACACAGCGCTTCCCTCGAAGCTCCCTCGTG 3240

Db 582 TGGGAAACCCGACAGACTATTAAGATCCAGGGCGTTTCCCCCTGGAAAGCTCCCTCG56 641

642	CGGCTTCCTCGTTCGACCCGTGCGCTTACCGGATACCTGTCCGCTTCTCCCTCGGGA	701
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QY 3301 AGCGTGGCGCTTTCTCATAGCTACGCTGTAGATATCTCAGTTCCGCTGTAGGTCCTGCC 3360

DH 702 AGCGTAGCGCTTTCTCATAGCTACGCTGTAGATATCTCAGTTCCGCTGTAGGTCCTGCC 761

3361 TCCAGCTGGGCTGTGTGACGAAACCCCGGTTAGCCCGACCGCTGGCCTTATCCGGT 3420

Db	762	TCCAGCTGGGCTGTGTGACGAAACCCCGTTACGCCCGACCGCTGGGCTTATCCGCT	821
Ov	3421	AACATATGTTTGAGTCCAAACCCGGTAGACACAGACTTATCGCAGCTGGCAGAGCCACT	3480

Db 822 AACTATCGTCTTGAGTCCAAACCCGGTAGACACGACTTATTCGCCACTGGCAGCAGCCACT 881

QY 3481 GGTAACAGATTAGCAGACCGAGTATGAGCGGTGCTACAGAGTTCCTGAAGTGTGTG 3540

Db 882 GGTAACAGATTAGCAGACCGAGTATGAGCGGTGCTACAGAGTTCCTGAAGTGTGTG 941

3541 CCTAACTACGGCTACCTAGAGAAGC-AGTATTGGTATCTGGCTCTGCTGAAGCCAGT 3599

Db 942 CCTAACTACGGCTACACTAGAAAGCAAGATTATTGTTATCTGGGCTCTGCTGAAACCAAT 1001

Db 1002 TACCTTCGAAAAAAGTTGGTAGCTCTTGAATCCGCAAAAAAAC 1048

RESULT 12
CK281799/c
2003-12-01
FSC 02 NYC-2004

LOCUS	Accession	Gene	Library
CK291/199	933 DP	mRNA	linear
EST754513	Nicotiana benthamiana mixed tissue	CDNA	EST 02-ROG-2004
DEFINITION	normalized, full-length Nicotiana benthamiana	CDNA	clone NBMC477 5'

Accession end, tRNA sequence.
 CK291799
 Version CK291799.1 GI:39872608
 Yarnwddpc bam

LEWIS
ALWORLD
SOURCE
Nicotiana benthamiana

ORGANISM

Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.

REFERENCE

1 (bases 1 to 933)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
Generation of EST sequences from *Nicotiana benthamiana*

JOURNAL COMMENT

Unpublished (2003)
Other ESTs: EST754514
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source
Location/Qualifiers

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/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBW477"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;
supplier: RNA was isolated from *Nicotiana benthamiana*
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (*Pseudomonas syringae* pv. tomato 12 hr;
Xanthomonas campestris pv. *campestris* 12 hr, 18hr;
Pseudomonas syringae pv. *phaseolicola* 18hr, and *Xanthomonas*
campestris pv. *vesicatoria* 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Query Match 16.8%; Score 886.4; DB 7; Length 933;
Best Local Similarity 99.9%; Pred. No. 1.8e-243;
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 933 GCCCAACCTTTCATAGAAAGCGGCGTGAATCGAAATCTGTGATGCGAGTTGGCGCT 874
QY 4104 CGCTTGTGGTCAATTCGAAAGCCCAAGATCCGCTCGAAGAACTGCTCAAGAAAGCGA 4163
Db 873 CGCTTGTGGTCAATTCGAAAGCCCAAGATCCGCTCGAAGAACTGCTCAAGAAAGCGA 814
QY 4164 TAGAAGCGATGCGCTCGATCGGAGCGCGATACCGTAAACAGAGAAAGCGGTCA 4223
Db 813 TAGAAGCGATGCGCTCGATCGGAGCGCGATACCGTAAACAGAGAAAGCGGTCA 754
QY 4224 GCCCATTCGCGCGCAAGCTTTCAGCAATATCAGCGGTAGCAACGCTATGTCTGTATAG 4283
Db 753 GCCCATTCGCGCGCAAGCTTTCAGCAATATCAGCGGTAGCAACGCTATGTCTGTATAG 694
QY 4284 CGGTCCGCCACACCCAGCGCGCCAGTTCGATGAAATCAGAAAAAGCGGCATTTTCCACC 4343
Db 693 CGGTCCGCCACACCCAGCGCGCCAGTTCGATGAAATCAGAAAAAGCGGCATTTTCCACC 634
QY 4344 ATGATATTCGCGCAAGCGAGATCGCATGCGTCAAGAGATCTCGCGTGGGGATG 4403
Db 633 ATGATATTCGCGCAAGCGAGATCGCATGCGTCAAGAGATCTCGCGTGGGGATG 574
QY 4404 CGGCGCTTGAAGCTCGGGAACAGTTGGCTGCGCGGAGCCCTTATGCTCTTCCAGA 4463
Db 573 CGGCGCTTGAAGCTCGGGAACAGTTGGCTGCGCGGAGCCCTTATGCTCTTCCAGA 514

QY 4464 TCATCTGATGACAAAGACCGGCTTCCATCCAGTAGTGTCGCTCGATCGATGTTTC 4523
Db 513 TCATCTGATGACAAAGACCGGCTTCCATCCAGTAGTGTCGCTCGATCGATGTTTC 454
QY 4524 GCTTGTGTGTAATGAGGACAGTATGCGGATCAAGCGTATGACAGCGCCCGCATTCATCA 4583
Db 453 GCTTGTGTGTAATGAGGACAGTATGCGGATCAAGCGTATGACAGCGCCCGCATTCATCA 394
QY 4584 GCCATATGATATCTTTCTCGGCGAGAGCAAGGTGATATGACAGAGATCTTCCCGCGC 4643
Db 393 GCCATATGATATCTTTCTCGGCGAGAGCAAGGTGATATGACAGAGATCTTCCCGCGC 334
QY 4644 ACTTCGCCATATGACAGCGAGTCCCTTCCGCTTCACTGACAAAGTGAAGAGAGTGGC 4703
Db 333 ACTTCGCCATATGACAGCGAGTCCCTTCCGCTTCACTGACAAAGTGAAGAGAGTGGC 274
QY 4704 CAAGAAAGCCCGCTGTGTGAGCAGGACAGATAGCCGCTGCTGTGCTGAGATTTCATTC 4763
Db 273 CAAGAAAGCCCGCTGTGTGAGCAGGACAGATAGCCGCTGCTGTGCTGAGATTTCATTC 214
QY 4764 AGGCGACCGGACAGGTGTGTTGACAAAAGAACCGGGGCGCCCTGCGTGAAGCGCG 4823
Db 213 AGGCGACCGGACAGGTGTGTTGACAAAAGAACCGGGGCGCCCTGCGTGAAGCGCG 154
QY 4824 AACACGCGGATCAGACGAGCGGATGCTGTTGTCGCGCATATGCGGAATAGCCTC 4883
Db 153 AACACGCGGATCAGACGAGCGGATGCTGTTGTCGCGCATATGCGGAATAGCCTC 94
QY 4884 TCACCCAGACCGGCGGAGAACCTGCTGCAATCATCTTGTTCATTC 4931
Db 93 TCACCCAGACCGGCGGAGAACCTGCTGCAATCATCTTGTTCATTC 46

RESULT 13

CV983341 951 bp mRNA linear EST 30-NOV-2004
LOCUS CV983341
DEFINITION UMC-boef 0A01-002-g06 Ovarian Follicle boef Bos taurus cDNA 3', mRNA
sequence.

ACCESSION CV983341 GI:56144062
VERSION CV983341.1
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus

ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.

REFERENCE

1 (bases 1 to 951)
Prather, R.S., Antoniou, E., Garverick, H.A., Green, J.A., Lucy, M.C.,
Roberts, R.M., Smith, M.F. and Youngquist, R.S.
USDA Grant NRI-2002-03476; Bovine ESTs: Focus on Female
Reproduction

JOURNAL COMMENT

Unpublished (2002)
Contact: DNA Core Facility (Bovine Project)
Animal Science - RS Prather
University of Missouri-Columbia
Mell Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573)882-0428
Fax: (573)884-5552
Email: bovine@rnet.missouri.edu
POLYA=No.

FEATURES

source

Location/Qualifiers

1..951
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/dev_stage="Ovarian Follicle"
/note="Vector: pSPORT1; Funding: The production of ESTs
submitted in this project was funded by USDA Grant
MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female
Reproduction' to RS Prather (Primary Investigator), E
Antonou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF
Smith and RS Youngquist. Genetic Source: Heifers for the

project were purchased from <http://www.circleranch.com/home.html>, Iberia, MO (<http://www.circleranch.com/home.html>). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: <http://genome.mnrc.msu.edu/Bovine/Methods.html>. Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAR-60 reagent (Tel-Test, Friendswood, TX) and the poly(N) + RNA was obtained by two rounds of purification with the Oligetex mRNA Isolation Kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the Superscript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A) + RNA was annealed at 37 degrees with 10mcg of NotI-tag-dT18 oligonucleotide (GCTGCTCGGCGGC-tag-T18) and reverse transcribed at 37 degrees with Superscript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (<http://genome.uowm.edu/pubsoft/software.html>) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and Kase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dT18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dT oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary library characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence

QY		3561	AAGAACAGATTGGATCTGGCGTGTGTAAGCAGTTACCTTCGAAAAAGAGTTGG	362
Db		662	AAGAACAATTGGATCTGGCGTGTGTAAGCAGTTACCTTCGAAAAAGAGTTGG	721
QY		3621	TAGCTCTTGATCCGGCAACAACACCGCTGTAAGCGGTGGTTTTTTTGGTTGGAGACA	3680
Db		722	TAGCTCTTGATCCGGCAACAACACCGCTGTAAGCGGTGGTTTTTTTGGTTGGAGACA	781
QY		3681	GCAATTTACGCCAAGAAAAAAAAAGATCTTCAGAAAGATCTTTTCTTACGGGGTC	3740
Db		782	GCAGATTACGCCAAGAAAAAAAAAGATCTTCAGAAAGATCTTTTCTTACGGGGTC	841
QY		3741	TGACCGTAGTGAACGAATACTACGTTAAGGAT-TTGGTCAATGAGATTATC	3794
Db		842	TGACCGTAGTGAACGAATACTACGTTAAGGANNATTGGTCAATGAGATTATC	896
 RESULT 14 CB686151/c				
LOCUS DEFINITION CB686151 mRNA linear EST 09-Apr-2003				
CB686151 Bn01b_02008.A 925 bp				
Bn01b_AAPC_ECORC transgenic Brassica napus overexpressing BNCP17 cDNA clone Bn01b_02008, constitutively frost_tolerant Brassica napus cDNA clone Bn01b_02008, mRNA sequence.				
CB686151				
ACCESSION		CB686151.1	GI:29689876	
VERSION		EST.		
KEYWORDS		Brassica napus (rape)		
SOURCE		Brassica napus		
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosidae; eurosidae II; Brassicales; Brassicaceae; Brassica.		
REFERENCE		1 (bases 1 to 925) Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A., Chagnon,J., Farah,S., Couroux,P. and Hattori,J.		
AUTHORS		Expressed Sequence Tags from constitutively frost tolerant transgenic Brassica napus overexpressing BNCP17 unpublished (2002)		
TITLE		Contact: Singh,J.A.		
JOURNAL		Eastern Cereal and Oilseed Research Centre Agriculture and Agri-food Canada		
COMMENT		KW Neelby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA 0C6, Canada		
		Tel.: (613) 759-1662		
		Fax: (613) 759-1701		
		Email: singhj@agr.gc.ca.		
FEATURES		location/Qualifiers		
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		/dev_stage="3 weeks seedling grown at room temperature"		
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		/note="Vector: Bluescript SK+/XhoI-EcoRI Site 1: EcoRI; Site 2: XhoI; Germinated in soil flats and seedlings grown for 3 weeks in a Conviron E-15 cabinet set at 20°C /16 hr light (250 Em-2sec-1) and 16 °C / 8 hr dark. Fourth leaves collected at 9 am and immediately frozen."		
 ORIGIN				
Query Match		16.6%	Score 875;	DB 6; Length 925;
Best Local Similarity		98.6%	Pred. No. 3.4e-240;	
Matches		886; Conservative	6; Mismatches	6; Indels 1; Gaps 1;
QY		2701	GGTGTCTAGAGCATCATGCTCATAGCTGTTTCTCTGTGAAAATTGTTATCCGCTACA	2760
Db		898	GCGGCGTTGGGATATCATGCTCATAGCTGTTT-CTGTGTAAATTTGTTATCCGCTACA	840
QY		2761	ATTCCACAACAATTCAGCCGGAAGCATTAAGTGTAAAGCTGGGGTGCTTAATGAGTG	2820

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
Db		839	ATTCCACA	CAACATACGAGCCGGAAGCATTAAGTGAAGCTTGAGGCTGCTTAATGAGTGG	780				
Qy		2821	AGCTAACT	CAACATTAATGCGTTGGCGCTCACATGCCCGCTTTCACAATCGGAAACCTGTGCG	2880				
Db		779	AGCTAACT	CAACATTAATGCGTTGGCGCTCACATGCCCGCTTTCACAATCGGAAACCTGTGCG	720				
Qy		2881	TGCCAGCT	GCATTAATGAATGCGCCCAACGCGCGGGGAGAGGCGGTTTGCATATTGGGCGC	2940				
Db		719	TGCCAGCT	GCATTAATGAATGCGCCCAACGCGCGGGGAGAGGCGGTTTGCATATTGGGCGC	660				
Qy		2941	TCTTCCGCTT	CTCGCTCACTGCACTTCGCTGGGCTCGCTTCCTTCCGCTGCGGCGAGCGGTA	3000				
Db		659	TCTTCCGCTT	CTCGCTCACTGCACTTCGCTGGGCTCGCTTCCTTCCGCTGCGGCGAGCGGTA	600				
Qy		3001	TCAGCTCACT	CAAAAGGCGGTAAATACGTTATCCACAGAAATAGAGGGATATAGCAGAGAAAG	3060				
Db		559	TCAGCTCACT	CAAAAGGCGGTAAATACGTTATCCACAGAAATAGAGGGATATAGCAGAGAAAG	540				
Qy		3061	AACATGTG	GAGCAAAAAGGCCAGCAAAAAGGCCAGAAACCGTAAAAAAGCCGCGTGTGCGC	3120				
Db		539	AACATGTG	GAGCAAAAAGGCCAGCAAAAAGGCCAGAAACCGTAAAAAAGCCGCGTGTGCGC	480				
Qy		3121	TTTTTCCAT	GAGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGC	3180				
Db		479	TTTTTCCAT	GAGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGC	420				
Qy		3181	TGGCGAAA	CCCCGACAGGACTTAATGAATACAGAGGCGTTCCCGCTGGAAGCTCCCTCGTG	3240				
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Qy		3241	CGCTCTCT	CTCTTCGCAACCTTCGCGCTTAACCGGATACGTTCCGCTTTCCTTCGCGGA	3300				
Db		359	CGCTCTCT	CTCTTCGCAACCTTCGCGCTTAACCGGATACGTTCCGCTTTCCTTCGCGGA	300				
Qy		3301	AGCGTGGG	CGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTTGGGTAGAGTGGTTCGC	3360				
Db		299	AGCGTGGG	CGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTTGGGTAGAGTGGTTCGC	240				
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Db		239	TCCAAAGCT	GAGGCTGTGTGACAGAAACCCCGGTTAGCGCCGACGCGCTGACCTTAATCCGGT	180				
Qy		3421	AACATAGT	CGTCTTGAAGTCCAACCCCGGTAAAGACACACACTTATCGCAGCTGGACAGCCACT	3480				
Db		179	AACATAGT	CGTCTTGAAGTCCAACCCCGGTAAAGACACACACTTATCGCAGCTGGACAGCCACT	120				
Qy		3481	GGTAAACG	AGATTAGCAAGACGAGGTATATAGGCGGTCTACAGAGTTCTTGAAGTGGTG	3540				
Db		119	GGTAAACG	AGATTAGCAAGACGAGGTATATAGGCGGTCTACAGAGTTCTTGAAGTGGTG	60				
Qy		3541	CCTAACTA	ACGGCTACACTAGAAAGAACAGTATTGGTATCTGCGGCTCTGCAAGCCAGT	3599				
Db		59	CCTAACTA	ACGGCTACACTAGAAAGAACAGTATTGGTATCTGCGGCTCTGCAAGCCAGT	1				
RESULT 15									
LOCUS		CP269652							
DEFINITION		CP269652	1073 bp	mRNA	linear	EST 13-AUG-2003			
ACCESSION		CP269652							
VERSION		CP269652.1							
KEYWORDS		EST.							
SOURCE		Fragiliariopsis cylindrus							
ORGANISM		Fragiliariopsis cylindrus							
REFERENCE		1							
AUTHORS		Mock T. and Valentin K.							
TITLE		EST analysis of freezing tolerance in the Antarctic diatom							
		Fragiliariopsis cylindrus: Detection of numerous cold adaptation							
		related genes and gene transfer events							

JOURNAL COMMENT

Unpublished (2003)
 Contact: Mock T
 Biological Oceanography
 Alfred-Wegener-Institute for Polar and Marine Research
 Am Handelshafen 12, D-27570 Bremerhaven, Germany
 Tel: +49 471 4831 1893
 Fax: +49 471 4831 1425
 Email: tmock@awi-bremerhaven.de
 Sequence with unknown function
 PCR Primers
 FORWARD: 5'lambdaTriplex2
 BACKWARD: 3'lambdaTriplex2
 Seq primer: ctgggaagcgccatcggtgtgt.
 Location/Qualifiers

FEATURES

source

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 /db_xref="taxon:186039"
 /clone_id="Fragilariopsis cylindrus SMART cDNA library (Clontech)"
 /note="Vector: pTriplex2; total polyA was used for first-strand synthesis with SMART IV oligos and CDS 11/3'PCR primer. Double strand cDNA synthesis was done by LD PCR using the following program: 95oc for 5 min denaturation and subsequent 20 cycles at 95oc (2min) and 68oc (6min). After SfiI digestion the cDNA was fractionated with CHROMA Spin-400 columns. These cDNAs were ligated overnight into pTriplex2 vectors."

ORIGIN

Query Match 16.4%; Score 866.2; DB 6; Length 1073;
 Best Local Similarity 96.4%; Fred. No. 1.3e-237;
 Matches 927; Conservative 0; Mismatches 28; Indels 7; Gaps 4;

QY 2839 GCGTTGCGCTCACTCCCGCTTTCAGTCGGGAAACCTGTCGCAAGCTCATTAATGA 2898
 DB 1 GCTTCTTGCTCACTCCCGCTTTCAGTCGGGAAACCTGTCGCAAGCTCATTAATGA 60

QY 2899 ATCGGCCAAGCGCGGGGAGAGCGGTTGCGTAATGGGCGCTCTTCCGCTTCTCGCTC 2958
 DB 61 ATCGGCCAAGCGCGGGGAGAGCGGTTGCGTAATGGGCGCTCTTCCGCTTCTCGCTC 120

QY 2959 ACTGACTGCTGCGCTCGCTGCTGCTGCGGCGAGCGGATCAGCTCACTCAAGGCG 3018
 DB 121 ACTGACTGCTGCGCTCGCTGCTGCTGCGGCGAGCGGATCAGCTCACTCAAGGCG 180

QY 3019 GTAATACGGTTATCCACAGAAATCAGGGGATACGACAGAAAGAAACATGTGACAAAGGC 3078
 DB 181 GTAATACGGTTATCCACAGAAATCAGGGGATACGACAGAAAGAAACATGTGACAAAGGC 240

QY 3079 CAGCAAAAGCCAGAAACCGTAAAGGCGGTTGCTGCGCTTTTTCATAGGCTCCGC 3138
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QY 3139 CCCCCGAGAGCATCAAAAATGACGCTCAAGTCAGAGGTGCGAAACCCGACAGGA 3198
 DB 301 CCCCCGAGAGCATCAAAAATGACGCTCAAGTCAGAGGTGCGAAACCCGACAGGA 360

QY 3199 CTATAAAGATACAGGCGTTTCCCTGGAGCTCCCTGCGCTCTCTGTTCCGACC 3258
 DB 361 CTATAAAGATACAGGCGTTTCCCTGGAGCTCCCTGCGCTCTCTGTTCCGACC 420

QY 3259 CTGCGGCTTACCGGATACCTGTCGCTTCTCCCTGGGAAAGGCGGCTTCTCAT 3318
 DB 421 CTGCGGCTTACCGGATACCTGTCGCTTCTCCCTGGGAAAGGCGGCTTCTCAT 480

QY 3319 AGCTCAGCTGTAGTATCTCAGTTGCTGTAGTGTGCTTCCAGCTGAGCTGTGTG 3378
 DB 481 AGCTCAGCTGTAGTATCTCAGTTGCTGTAGTGTGCTTCCAGCTGAGCTGTGTG 540

QY 3379 CAGGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGTAATATGTCTTAGATCC 3438

DB 541 CAGGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGTAATATGTCTTAGATCC 600

QY 3439 AACCGGTAAAGACAGACTTATGCGCACTGCGACAGCACTGTAAACAGATTAGCAGA 3498

DB 601 AACCGGTAAAGACAGACTTATGCGCACTGCGACAGCACTGTGTAAACAGATTAGCAGA 660

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QY 3557 CTAGAAGACA-GTATTTGGTATCT-GCGCTGCTGTAAGCC--AGTTACTTCGAAA 3611

DB 721 CTAGAAGACAGTATTTGGTATCTGCTGCTGTAAGCCAGTAACTTCGAAA 780

QY 3612 AAGAGTTGTAGTCTTGAATCCGCAACAAACCAACCGCTGTAGCGGTGTTTTGT 3671

DB 781 AAGAGTTGTAGTCTTGAATCCGCAACAAACCAACCGCTGTAGCGGTGTTTTGT 840

QY 3672 TTGCAAGCAGAGATTACGCGCAGAAAAGATCTCAAGAAGATCCTTGTATCTTTC 3731

DB 841 TTGCAAGCAGAGATTACGCGCAGAAAAGATCTCAAGAAGATCCTTGTATCTTTC 900

QY 3732 TACGGGTTGACGCTCACTGAGAACGAAATCTACGTTAAGGATTTTGTATGAGATT 3791

DB 901 TACGGGTTGACGCTCACTGAGAACGAAATCTACGTTAAGGATTTTGTATGAGATT 960

QY 3792 AT 3793

DB 961 AT 962

Search completed: May 14, 2006, 02:13:03
 Job time : 12713 secs

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| | | | |
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QY 3306 GGGCGTTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTCCGTTGAGTCCGTTCCGCTCAA 3365
| | | | |
Db 6511 GGGCGTTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTCCGTTGAGTCCGTTCCGCTCAA 6570
QY 3366 GCTGGGCTGTGTGACGAAACCCCGCTTACGCCGAGCCGCTGCGCTTATCCGGTAACTA 3425
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Db 6571 GCTGGGCTGTGTGACGAAACCCCGCTTACGCCGAGCCGCTGCGCTTATCCGGTAACTA 6630
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| | | | |
Db 7025 -----TT 7026
QY 3966 GGGGTGGGCGAAGAACTTCAGCATAGAGTCCCGCGCTGAGGATCATCAGCGGCGTTC 4025
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 Db 8287 TTCTACGTTCCGCTTCTTTAGCAGCCCTTGCGCCCTGAGTGTCTTGGCAGCGT 8344

RESULT 2
 US-09-554-929-1/c
 ; Sequence 1, Application US/09554929
 ; Patent No. 6521427
 ; GENERAL INFORMATION:
 ; APPLICANT: Evans, Glen A.
 ; TITLE OF INVENTION: A Method for the Complete Chemical
 ; FILE REFERENCE: P-EA 4749
 ; CURRENT APPLICATION NUMBER: US/09/554, 929
 ; NUMBER OF SEQ ID NOS: 193
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 4800
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic plasmid
 US-09-554-929-1

Query Match 33.9%; Score 1793.4; DB 3; Length 4800;
 Best Local Similarity 91.8%; Pred. No. 0;
 Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1;

Qy 3127 CATAGGCTCGGCCCCCTGAGAGCATCAAAATGAGCCCTCAAGTCAGAGTGGCGA 3186
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 Db 4740 AACCCGACAGGACTATAAGATACAGGCGTTTCCCTGAGAGTCCCTGTCGCTCT 4681
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 Db 4560 CTGGGCTGTGACGAAACCCCGCTTCAAGCCGACCGCTGCGCTTATCCGCTAAC 4501
 Qy 3427 CCGTTCGATCCAAACCGGTGAAGACGACTTATCGCACTGGACAGCCACTGTTAC 3486
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 Qy 3667 TTGTTTGAAGCAGATTAAGCGGAGAAAGAAAGATCTCAAGAGATCTTTGATC 3726
 Db 4260 TTGTTTGAAGCAGATTAAGCGGAGAAAGAAAGATCTCAAGAGATCTTTGATC 4201

Qy 3727 TTTTCTACGGGCTGACGCTCAGTGAACGAAACTCACTTAAGGATTTGGTCAATG 3786
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 Qy 3787 AGATTATCTGACCAAGCGGCAATGTCCTCCCACTTCGCAATTCGCGGCGCATG 3846
 Db 4141 ----- 4142
 Qy 3847 ATGGCGGATAGCCGCTGCTGTTTCTCGAATGCCGACGATTTGCACTGCCGATAGAC 3906
 Db 4141 ----- 4142
 Qy 3907 TCCGCGAGTGTGTCAGCCTCAGGACGAGCTGAACCAACTCGGAGGGAGTCGAGCCG 3966
 Db 4141 -----GCCCC 4137
 Qy 3967 GGGTGGCGAAGAACTCAGCATGATATCCCGGCTGAGAGATCATCAGCCGCGTCC 4026
 Db 4136 GGGTGGCGAAGAACTCAGCATGATATCCCGGCTGAGAGATCATCAGCCGCGTCC 4077
 Qy 4027 CGGAAACGATTCGGAAGCCCACTTTCATGAAAGCGGCGGTGGAATCGAAATCTCGT 4086
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 Qy 4507 GCTCGATGCGATGTTTCTGCTGATGCAATGGGCGAGTATGCGGATCAAGCGTATGCA 4566
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 Qy 4567 GCGCGCGCATTTGATCAGCCATGATGATATCTTTCTCGGCGAGGACAGGTGATGACA 4626
 Db 3536 GCGCGCGCATTTGATCAGCCATGATGATATCTTTCTCGGCGAGGACAGGTGATGACA 3477
 Qy 4627 GGAATTCCTGCCCCCGGACTTGGCCCAATGAGCGGAGTCCCTTCCGCTTCAGTGA 4686
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 Qy 4687 CGTGAGCAGAGCTGCGCAAGAAACCGCTGCTGAGCCAGCAGATGAGCCGCTGCT 4746
 Db 3416 CGTGAGCAGAGCTGCGCAAGAAACCGCTGCTGAGCCAGCAGATGAGCCGCTGCT 3357
 Qy 4747 CGTCTGCAATTTATTCAGGCGACCGGACAGGTGCGTCTTGAACAAAGAAACCGGCGCC 4806
 Db 3356 CGTCTGCAATTTATTCAGGCGACCGGACAGGTGCGTCTTGAACAAAGAAACCGGCGCC 3297
 Qy 4807 CTTGCGCTGACAGCCGGAACACGCGCGCATCAGAGCAGCGGATGCTGTGTGCCAGT 4866

Db 3296 CCGGCGGTGACACCGGAGACCGGCGCATCAGAGACCGGATGCTGTGCGCCAGT 3237
QY 4867 CATAGCGGATAGACCTCTCCACCCAGGCGCGGAGAACCTGTGCAATCCATCTTGT 4926
Db 3236 CATAGCGGATAGACCTCTCCACCCAGGCGCGGAGAACCTGTGCAATCCATCTTGT 3177
QY 4927 CAATCATGCGAAAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4986
Db 3176 CAATCATGCGAAAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3117
QY 4987 AGATCTTGGCGGCGGAGAAAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5046
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QY 5047 AGGCGCGCCGACGCTGGCAATTCGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTG 5106
Db 3056 AGGCGCGCCGACGCTGGCAATTCGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTG 2997
QY 5107 ATGCGCATGTAGGCGCATCTGCAAGCTACCTGCTTCTCTTGGCGCTTGCCTTTC 5166
Db 2996 ATGCGCATGTAGGCGCATCTGCAAGCTACCTGCTTCTCTTGGCGCTTGCCTTTC 2937
QY 5167 TCCAGATAGCCGAGTACGATCATTCATCCGCGGCTGACACCGTTTTCGCGACTGGCT 5226
Db 2936 TCCAGATAGCCGAGTACGATCATTCATCCGCGGCTGACACCGTTTTCGCGACTGGCT 2877
QY 5227 TCTACGTGTTCGCTCTCTTATGAGCGCTTGGCGCGCTGAGTGTGCTGCGGACGCTG 5283
Db 2876 TCTACGTGTTCGCTCTCTTATGAGCGCTTGGCGCGCTGAGTGTGCTGCGGACGCTG 2820

RESULT 3

US-09-380-190A-29/c
Sequence 29, Application US/09380190A

Patent No. 6410220

GENERAL INFORMATION:

APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.

TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES

THEREOF

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUEHLING, RAASCH & GRUBHARDT, P.A.

CITY: MINNEAPOLIS

STATE: MINNESOTA

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,190A

FILING DATE: 26-Aug-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US98/03918

FILING DATE: 28-FEB-98

ATTORNEY/AGENT INFORMATION:

NAME: MUEHLING, ANN M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 228, 00010201

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-305-1217

TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 5594 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-380-190A-29

Query Match 31.3%; Score 1652.4; DB 3; Length 5594;
Best Local Similarity 85.4%; Pred. No. 0;
Matches 1916; Conservative 0; Mismatches 261; Indels 67; Gaps 4;

QY 3107 CCGCGTGTGCGCGCTTTTTCATAGGCTCCGCCCTGACGAGCATCACAAAATCGAC 3166
Db 5591 CGGCGTGTGCGCGCTTTTTCATAGGCTCCGCCCTGACGAGCATCACAAAATCGAC 5532
QY 3167 GCTCAATGACAGGTGGCGAAACCCGACAGAGCTATAAGATACGAGCGTTCCCTG 3226
Db 5531 GCTCAATGACAGGTGGCGAAACCCGACAGAGCTATAAGATACGAGCGTTCCCTG 5472
QY 3227 GAAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3286
Db 5471 GAAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5412
QY 3287 TTTCTCCCTTGGGAAAGCGTGGCGCTTTCTCATAGCTCAAGCTGATGATCTGAGTCCG 3346
Db 5411 TTTCTCCCTTGGGAAAGCGTGGCGCTTTCTCATAGCTCAAGCTGATGATCTGAGTCCG 5352
QY 3347 TGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3406
Db 5351 TGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5292
QY 3407 GCGCTTATCCGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3466
Db 5291 GCGCTTATCCGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5232
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QY 3975 GAAGAACTCAGCATGAGATCCCGCGCTGAGAGATCATCAGCGCGCTCCCGGAAAC 4034
Db 4691 TTTGGCCCATATTCAGGTGTTTCATCTGTTCTGACCTTGAATGAACTTCTATTC 4632
QY 4035 GATTCGAAAGCCCAACTTTCATAGAAAGCGGAGTGAATGAAATCTCG----- 4085

Db 4631 AGTATGATATTTTCCATGCTTGCAAAAATGGCGTACTTAAGCTAGCTTGCCAAACCTTA 4572
4086 -----TGATGGCAGGTTGGCGCTGGCTTGTCGTCATT 4119
Db 4571 CAGGTGGGCTTTTCAATTCCTCCCTTTTCTGGAGGTGGCGCTGCTTGTCGTCATT 4512
4120 TCGAACCCCAAGTCCCGCTCAGAAAGAACTCGTCAAGAAAGCGCATAGAAAGCGATCGCT 4179
Db 4511 TCGAACCCCAAGTCCCGCTCAGAAAGAACTCGTCAAGAAAGCGCATAGAAAGCGATCGCT 4452
4180 GCGAATCGGAGGCGCGGATACCGTAAAGCAAGAGAGCGGTGACCCATTGCGCGCA 4239
Db 4451 GCGAATCGGAGGCGCGGATACCGTAAAGCAAGAGAGCGGTGACCCATTGCGCGCA 4392
4240 GCTCTTAGCAATATCAGGGGTAGCCAAAGCTATGCTCCTGATAGCGGTCCGCCAACCCA 4299
Db 4391 GCTCTTAGCAATATCAGGGGTAGCCAAAGCTATGCTCCTGATAGCGGTCCGCCAACCCA 4332
4300 GCGGCGCAGTGCATGATGATCCAGAAAGCGGCAATTTTCCACATGATATTGCGCAAGC 4359
Db 4331 GCGGCGCAGTGCATGATGATCCAGAAAGCGGCAATTTTCCACATGATATTGCGCAAGC 4272
4360 AGGCATTCGCGATGGGTCAAGCAAGATCTGCGCGTGGGCAATGCGCGCTTGAAGCTGG 4419
Db 4271 AGGCATTCGCGATGGGTCAAGCAAGATCTGCGCGTGGGCAATGCGCGCTTGAAGCTGG 4212
4420 GCGAAGTTCCGCGTGGCGGAGCCCTGATGCTCTTCCGTCAGATCATCTCTATGACAA 4479
Db 4211 GCGAAGTTCCGCGTGGCGGAGCCCTGATGCTCTTCCGTCAGATCATCTCTATGACAA 4152
4480 GACCGGCTTCCATCCGAGTACGTGCTGCTCGATGCGATGTTGCTGGTGGTGCATG 4539
Db 4151 GACCGGCTTCCATCCGAGTACGTGCTGCTCGATGCGATGTTGCTGGTGGTGCATG 4092
4540 GCGAGTACCGCGATGCAAGCGTATGCAAGCGCGCGCATGTCATGACCATGATGATCTT 4599
Db 4091 GCGAGTACCGCGATGCAAGCGTATGCAAGCGCGCGCATGTCATGACCATGATGATCTT 4032
4600 TCTCGGCGAGGAGCAAGGTGAGTGAAGAGATCTTCCGCGCGCACTTCCGCCATATGA 4659
Db 4031 TCTCGGCGAGGAGCAAGGTGAGTGAAGAGATCTTCCGCGCGCACTTCCGCCATATGA 3972
4660 GCGAGTACCGCGTCCGCTCAGTGAACAAGTGCAGAGCAAGCTGCGAAGGAAAGCGCGTGG 4719
Db 3971 GCGAGTACCGCGTCCGCTCAGTGAACAAGTGCAGAGCAAGCTGCGAAGGAAAGCGCGTGG 3912
4720 TGGCGAGCGACGATAGCGCGCTGCTGCTGCTGATTCATTCAGGGCAACCGACAGT 4779
Db 3911 TGGCGAGCGACGATAGCGCGCTGCTGCTGCTGATTCATTCAGGGCAACCGACAGT 3852
4780 GCGTCTTGAACAAAAGAACCGGGCGCCCTGCGCTGAGACGCGGAAACCGCGGATCAG 4839
Db 3851 GCGTCTTGAACAAAAGAACCGGGCGCCCTGCGCTGAGACGCGGAAACCGCGGATCAG 3792
4840 AGCAGCGCATGCTGCTGCTGCGCGCATAGCGCATAGCCTTCCACCCAAAGCGGCG 4899
Db 3791 AGCAGCGCATGCTGCTGCTGCGCGCATAGCGCATAGCCTTCCACCCAAAGCGGCG 3732
4900 GAGAACTGCGTGAATCATCTTGTTCATCATGCGAAAGATCTGCTGCTCTT 4959
Db 3731 GAGAACTGCGTGAATCATCTTGTTCATCATGCGAAAGATCTGCTGCTCTT 3672
4960 GATCAGATCTTATGCTCCGCGCATGATCTTGGGGGCAAGAAAGCATCCAGTTTA 5019
Db 3671 GATCAGATCTTATGCTCCGCGCATGATCTTGGGGGCAAGAAAGCATCCAGTTTA 3612
5020 CTTTGCAGGCGCTCCCACTTACAGAGGCGCCCAAGCTGCGCAATTCGCGTTGCTTG 5079
Db 3611 CTTTGCAGGCGCTCCCACTTACAGAGGCGCCCAAGCTGCGCAATTCGCGTTGCTTG 3552
5080 CTGTTCATTAACCGCGCATGCTATGCGCATGTAAGCCCACTGCAAGCTACTGCT 5139

Db 3551 CTGTCCATTAACCGCGCATGCTAGCTATGCGCATGTAAGCCCACTGCAAGCTACTGCT 3492
4140 TTCTCTTGGCGCTGCGCTTTTCCCTTGTCCATATAGCCAGTATGATTCATTCGGG 5199
Db 3491 TTCTCTTGGCGCTGCGCTTTTCCCTTGTCCATATAGCCAGTATGATTCATTCGGG 3432
4200 GTACAGCCGCTTTCGCGGACTGCGCTTCTAGTGTGCTTCCCTTTAGACGCCCTTG 5259
Db 3431 GTACAGCCGCTTTCGCGGACTGCGCTTCTAGTGTGCTTCCCTTTAGACGCCCTTG 3372
4260 GCGTGAAGTCTTGGCGGAGCGGTG 5283
Db 3371 GCGTGAAGTCTTGGCGGAGCGGTG 3348

RESULT 4
US-09-380-190A-30/c
; Sequence 30, Application US/09380190A
; Patent No. 6410220
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
; THEREOF
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,190A
; FILING DATE: 26-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/03918
; FILING DATE: 28-FEB-98
; ATTORNEY/AGENT INFORMATION:
; NAME: MUEITING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 228,00010201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-380-190A-30

Query Match 30.6%; Score 1618.2; DB 3; Length 6561;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 1911; Conservative 0; Mismatches 23; Indels 269; Gaps 1;

4140 GCAAAAGCCGAGAAACGTAAGAAAGCGCGCTGCTGCTTTTTCATAGGCTCCGCC 3140
2305 GCAAGTGAATCTGAGGCGGCGCATCTCGCGGTGCTGCGCTTTTTCATAGGCTCCGCC 2246
3141 CCTGAGAGAGATACAAATAATGACGCTCAAGTCAAGAGTGGGAAACCCGAGAGACT 3200
2245 CCTGAGAGAGATACAAATAATGACGCTCAAGTCAAGAGTGGGAAACCCGAGAGACT 2186
3201 ATAAAGATACAGGCGTTTCCCTGGAAGCTCCCTGAGGCTCTCTGTTCCGACCT 3260

Db 2185 ATAAAGATACGAGCGCTTCCCTCGGAAAGCTCCCTGTCGCGCTCTCTGTTCCAGCCCT 2126
 QY 3261 GCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAG 3320
 Db 2125 GCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAG 2066
 QY 3321 CTCACGCTTACGATCTCAGTTCCGTTAGGTCGTTCCGTCGCAAGCTGCGCTTGTGCA 3380
 Db 2065 CTCACGCTTACGATCTCAGTTCCGTTAGGTCGTTCCGTCGCAAGCTGCGCTTGTGCA 2006
 QY 3381 CGAAGCCCGCTTCAAGCCGACCGCTGCGCTTATCCGTTAACTATCCCTTGAATCCAA 3440
 Db 2005 CGAAGCCCGCTTCAAGCCGACCGCTGCGCTTATCCGTTAACTATCCCTTGAATCCAA 1946
 QY 3441 CCCGGTAAAGACGACTATCGGCACTGCGACAGCACTGTATACAGATTTAGCAGAGC 3500
 Db 1945 CCCGGTAAAGACGACTATCGGCACTGCGACAGCACTGTATACAGATTTAGCAGAGC 1886
 QY 3501 GAGGTATGAGCGGTGCTACAGAGTTCTTGAAGTGTGCGCTTAACTACGCTACACTAG 3560
 Db 1885 GAGGTATGAGCGGTGCTACAGAGTTCTTGAAGTGTGCGCTTAACTACGCTACACTAG 1826
 QY 3561 AAGAACATTTTGTATCTGCGCTTGTCTGTAAGCAGTTA CTTTCGAAAAAGATTGG 3620
 Db 1825 AAGAACATTTTGTATCTGCGCTTGTCTGTAAGCAGTTA CTTTCGAAAAAGATTGG 1766
 QY 3621 TAGCTCTTATCCGCAACAAACACCGCTGATGAGCGTGTGTTTTTTTGTGCAAGCA 3680
 Db 1765 TAGCTCTTATCCGCAACAAACACCGCTGATGAGCGTGTGTTTTTTTGTGCAAGCA 1706
 QY 3681 GCAAGTTAGCGCGAAGAAAAAGATCTCAAGAAATCTTGTGATCTTTTCTACGGGTC 3740
 Db 1705 GCAAGTTAGCGCGAAGAAAAAGATCTCAAGAAATCTTGTGATCTTTTCTACGGGTC 1696
 QY 3741 TGACGCTCAGTGAAGCAAGAAACTCAGCTTAAAGGATTTTGTGATGAGATTCGTGAC 3800
 Db 1695 ---- 1696
 QY 3801 CAAAGCGGCATCGTGCCTCCCACTCTGCAATTGCGGGGCAATGATGCGCGATAGCC 3860
 Db 1695 ---- 1696
 QY 3861 GCTGCTGTTTCTGATTCGCGACGGAATTTGCACTGCGGTGAAGACTCCGCGAGTCTC 3920
 Db 1695 ---- 1696
 QY 3921 CAGCCTCAGGACGAGCTGAACCAACTCGGAGGGGATCGAGCCCGGGTGGCGAAGAA 3980
 Db 1695 ---- AATTCCGGGGTGGCGAAGAA 1675
 QY 3981 CTCACGATAGATCCCGGCTGAGAGATCATCAGCCGCGCTCCCGAAAAAGATTCC 4040
 Db 1674 CTCACGATAGATCCCGGCTGAGAGATCATCAGCCGCGCTCCCGAAAAAGATTCC 1615
 QY 4041 GAAGCCCAACCTTCAATGAAGCGCGGTGATGAATCTGCTGATGAGCGATTGGG 4100
 Db 1614 GAAGCCCAACCTTCAATGAAGCGCGGTGATGAATCTGCTGATGAGCGATTGGG 1555
 QY 4101 CGTGCCTGCTGATTCGAATCCAGAGTCCGCTCAGAAAGAACTCGTCAAGAAAG 4160
 Db 1554 CGTGCCTGCTGATTCGAATCCAGAGTCCGCTCAGAAAGAACTCGTCAAGAAAG 1495
 QY 4161 CGATTAAAGCGATGCGCTGCGAATGGAGCGCGGATACCGTAAAGCAAGAGAGCGG 4220
 Db 1494 CGATTAAAGCGATGCGCTGCGAATGGAGCGCGGATACCGTAAAGCAAGAGAGCGG 1435
 QY 4221 TCAGCCCATTCGCGCAAGCTCTTCAAGAAATACCGGTGAGCAAGCTTATGTCGTA 4280
 Db 1434 TCAGCCCATTCGCGCAAGCTCTTCAAGAAATACCGGTGAGCAAGCTTATGTCGTA 1375
 QY 4281 TAGCGGTCCGCAACCGCGCGCAAGTGAATCCAGAAAAAGCGGCAATTTCC 4340
 |||

Db 1374 TAGCGTCCGCAACCCAGCCGCGCACAGTGCATGAATCCAGAAAAAGCGGCATTTCC 1315
 QY 4341 ACCATGATATTCCGCAAGCAAGGCAATGCGCATGGGTCAACGAGATCTTCCGCTGGGC 4400
 Db 1314 ACCATGATATTCCGCAAGCAAGGCAATGCGCATGGGTCAACGAGATCTTCCGCTGGGC 1255
 QY 4401 ATGCGCGCTTGAAGCTGAGCAAGTTCGCTGAGCGAGAGCCCTGATGCTCTTGGTC 4460
 Db 1254 ATGCGCGCTTGAAGCTGAGCAAGTTCGCTGAGCGAGAGCCCTGATGCTCTTGGTC 1195
 QY 4461 AGATCATCTGATTCGAATCAAGAACCGGCTTCAATCCGAGTACGTCTGCTGATGATGT 4520
 Db 1194 AGATCATCTGATTCGAATCAAGAACCGGCTTCAATCCGAGTACGTCTGCTGATGATGT 1135
 QY 4521 TTGCTTGTGTCGATGAGGCGAGTACCGGATCAAGCGTATGCAAGCGCGCATTTGA 4580
 Db 1134 TTGCTTGTGTCGATGAGGCGAGTACCGGATCAAGCGGATGCAAGCGCGCATTTGA 1075
 QY 4581 TCAGCATGATGATTAATCTTCTGCGAAGACAAAGGTGAATGACAGAGATCTGCCCC 4640
 Db 1074 TCAGCATGATGATTAATCTTCTGCGAAGACAAAGGTGAATGACAGAGATCTGCCCC 1015
 QY 4641 GGCATTCGCGCAATGAGAGCGAGTCCCTCCGCTTCAAGTACAACTGAGCAGACT 4700
 Db 1014 GGCATTCGCGCAATGAGAGCGAGTCCCTCCGCTTCAAGTACAACTGAGCAGACT 955
 QY 4701 GCGCAAGAAACGCGCTGTCGACGACGATAGCCGCTGCTGCTGCAAGTTCA 4760
 Db 954 GCGCAAGAAACGCGCTGTCGACGACGATAGCCGCTGCTGCTGCAAGTTCA 895
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 Db 894 TTCAGGCGACCGGAGAGTGGCTTTGACAAAAAGAACTGGGCGCCCTGCTGACAGC 835
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 Db 834 CGGAACACGCGCGCATACAGAGCAGCGATTTGCTGTGAGCCAGTCAATGCGCAATGCC 775
 QY 4881 CTCTCACCAGCGCGCGAGAGACCTGCGTGAATTCATCTTGTCAATGCGAAGC 4940
 Db 774 CTCTCACCAGCGCGCGAGAGACCTGCGTGAATTCATCTTGTCAATGCGAAGC 715
 QY 4941 GATCCTCATCTGCTCTTGTGATCAGATCTGATTCATGATCCCGCGCATGATCTTGGCGGC 5000
 Db 714 GATCCTCATCTGCTCTTGTGATCAGATCTGATTCATGATCCCGCGCATGATCTTGGCGGC 655
 QY 5001 AAGAAAGCATCAGTTTACTTTGCAAGGCTTCCCACTTACAGAGAGGCGCCAGCT 5060
 Db 654 AAGAAAGCATCAGTTTACTTTGCAAGGCTTCCCACTTACAGAGAGGCGCCAGCT 595
 QY 5061 GGCATTCGCGTTCGCTTGTGCTGATTAACCGCCAGCTTACGCTATCGCATGTAAGC 5120
 Db 594 GGCATTCGCGTTCGCTTGTGCTGATTAACCGCCAGCTTACGCTATCGCATGTAAGC 535
 QY 5121 CCACTGCAAGCTACCTGCTTCTCTTTCGCTGAGTTTCCCTTTCGAGTATGAGCCAG 5180
 Db 534 CCACTGCAAGCTACCTGCTTCTCTTTCGCTGAGTTTCCCTTTCGAGTATGAGCCAG 475
 QY 5181 TAGCTGATTCATTCGCGGCTGACACCGTTTCTGCGAAGTGGCTTTCTAGTGTCCG 5240
 Db 474 TAGCTGATTCATTCGCGGCTGACACCGTTTCTGCGAAGTGGCTTTCTAGTGTCCG 415
 QY 5241 TTCTCTTGAAGCGCTTTCGCGCTGAGTGTGGGCAAGGCTG 5283
 Db 414 TTCTCTTGAAGCGCTTTCGCGCTGAGTGTGGGCAAGGCTG 372

RESULT 5
 US-08-472-809B-8
 ; Sequence 8, Application US/08472809B
 ; Patent No. 5925564
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwartz, Robert J.

Db 4562 AACCTGCAAGAAAGGCGATGAAAGGCGATCGCTGCGAATCGGGAAGGCGGATACGTTAA 4621
QY 4206 AGCAGAGAAAGCGGTCAAGCCATTCGCCCGCAAGCTCTTACAGAAATACAGGTAAGCC 4265
Db 4622 AGCAGAGAAAGCGGTCAAGCCATTCGCCCGCAAGCTCTTACAGAAATACAGGTAAGCC 4681
QY 4266 AACGCTTGTCTGATAGCGGTCCGCCACACCGAGCGGCGACAGTGTGATGAAATCCAGAA 4325
Db 4682 AACCTGATGCTGATAGCGGTCCGCCACACCGAGCGGCGACAGTGTGATGAAATCCAGAA 4741
QY 4326 AAGCGGCGATTTTCACCATGATATTTGGCAAGAGGCGATTCGCATGGGTCAAGACAGA 4385
Db 4742 AAGCGGCGATTTTCACCATGATATTTGGCAAGAGGCGATTCGCATGGGTCAAGACAGA 4801
QY 4386 TCCCTCGCGGTGGGCGATGCGCGCTTGAGCTTGCGCAAGTTTCGCTGCGCGAGCCCC 4445
Db 4802 TCCCTCGCGGTGGGCGATGCGCGCTTGAGCTTGCGCAAGTTTCGCTGCGCGAGCCCC 4861
QY 4446 TGATGCTCTTCTGTCAGATCATCTGATCGAAGAACCGGCTTCCATCCGATACGTGCT 4505
Db 4862 TGATGCTCTTCTGTCAGATCATCTGATCGAAGAACCGGCTTCCATCCGATACGTGCT 4921
QY 4506 CGCTCGATGCGATGTTTGGCTTGGTTCGATAGGCGAGGTAAGCGGATCAAGGTAAGC 4565
Db 4922 CGCTCGATGCGATGTTTGGCTTGGTTCGATAGGCGAGGTAAGCGGATCAAGGTAAGC 4981
QY 4566 AGCCGCGCATTTGATCATGAGCATGATGATGATCTTCTTCGAGAGAGCAAGGTGATGAC 4625
Db 4982 AGCCGCGCATTTGATCATGAGCATGATGATGATCTTCTTCGAGAGAGCAAGGTGATGAC 5041
QY 4626 AGGAGATCTTCGCGCGGCACTTTCGCGCAATAGCAAGCCAGTCCCTTCCGCTTCACTGACA 4685
Db 5042 AGGAGATCTTCGCGCGGCACTTTCGCGCAATAGCAAGCCAGTCCCTTCCGCTTCACTGACA 5101
QY 4686 AGCTGAGACACAGCTGCGGCGAAGAAAGCGCGGCGAGCAGCAGATGAGCGGCGTGC 4745
Db 5102 AGCTGAGACACAGCTGCGGCGAAGAAAGCGCGGCGAGCAGCAGATGAGCGGCGTGC 5161
QY 4746 TCGTCTGAGTTCATTCAGAGGACCGGACAGGTGCGTCTTGACAAAAAGAACCGGCGGC 4805
Db 5162 TCGTCTGAGTTCATTCAGAGGACCGGACAGGTGCGTCTTGACAAAAAGAACCGGCGGC 5221
QY 4806 CCTTCGCTGACAGCCGGAACACCGCGGCGATCAGAGCAGCCGATGTTGTTGGCCAG 4865
Db 5222 CCTTCGCTGACAGCCGGAACACCGCGGCGATCAGAGCAGCCGATGTTGTTGGCCAG 5281
QY 4866 TCATGAGCGAATAGCTCTTCAACCAAGCGGCGGAGAACTGCGTGCATTCATCTTGT 4925
Db 5282 TCATGAGCGAATAGCTCTTCAACCAAGCGGCGGAGAACTGCGTGCATTCATCTTGT 5341
QY 4926 TCAATCATGCGAAAGCATCTCATCTCTTCTTTCATGATCTTGATTCCTTCGCGCAT 4985
Db 5342 TCAATCATGCGAAAGCATCTCATCTCTTCTTTCATGATCTTGATTCCTTCGCGCAT 5401
QY 4986 CAGATCCTTGGGCGGCAAGAAAGCATTCAGTTTACCTTTCAGAGGCTTCCCAACTTACA 5045
Db 5402 CAGATCCTTGGGCGGCAAGAAAGCATTCAGTTTACCTTTCAGAGGCTTCCCAACTTACA 5461
QY 5046 GAGGCGCGCCAGCTGCGAATTCGAGTTTCGCTTGCATGATGAAACCGCGCATGTAAGC 5105
Db 5462 GAGGCGCGCCAGCTGCGAATTCGAGTTTCGCTTGCATGATGAAACCGCGCATGTAAGC 5521
QY 5106 TATGCGCATGTAAGCCCACTGCAAGTACCTGCTTCTTCTT 5146
Db 5522 AACTGTTGGGAAGGCGAATCGGTGCGGCTCTTTCGCTTAT 5562

RESULT 6
US-08-948-378A-7/c
; Sequence 7, Application US/08948378A
; Patent No. 6013258
; GENERAL INFORMATION:

APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Collins, Edward J.
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
TITLE OF INVENTION: THE HPV E7 PROTEIN
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 09-OCT-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/004001
TELEPHONE: 617-542-5070
TELEFAX: 617-543-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: PHOTOPHENV
US-08-948-378A-7
Query Match 29.7%; Score 1571.6; DB 3; Length 4665;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1850; Conservative 0; Mismatches 114; Indels 180; Gaps 3;
QY 3008 ACTCAAAAGGCGGTAATAGGTTATCCACAGATCAGGAGGATTAACGAGGAAAGAAACATGT 3067
Db 2624 AATGCAATGGGGAATACGGTTATCCACAGATCAGGAGGATTAACGAGGAAAGAAACATGT 2565
QY 3068 GAGCAAAAGGCGGCAAAAGGCGGAGAACCGTAAAGGCGGCTTGGCGTTTTC 3127
Db 2564 GAGCAAAAGGCGGCAAAAGGCGGAGAACCGTAAAGGCGGCTTGGCGTTTTC 2505
QY 3128 ATNAGCTCGCCCGCTGACAGACATCAAAAAATGAGCGTCAATCGAAGGTGGCGAA 3187
Db 2504 ATNAGCTCGCCCGCTGACAGACATCAAAAAATGAGCGTCAATCGAAGGTGGCGAA 2445
QY 3188 ACCGAGAGACTTAAGATACCAAGCGTTTCCCTGGAAGCTCCTGTCGCTCTC 3247
Db 2444 ACCGAGAGACTTAAGATACCAAGCGTTTCCCTGGAAGCTCCTGTCGCTCTC 2385
QY 3248 CTGTTCCGACCTTCGCTTACCGGATACCTGTCGCTTTCCTCTGGGGAAGGCTGG 3307
Db 2384 CTGTTCCGACCTTCGCTTACCGGATACCTGTCGCTTTCCTCTGGGGAAGGCTGG 2325
QY 3308 CGCTTTTCATAGTCAAGCTGTAAGTACTGAGTTCGAGTGAAGTGGTTCGCTCAAGC 3367
Db 2324 CGCTTTTCATAGTCAAGCTGTAAGTACTGAGTTCGAGTGAAGTGGTTCGCTCAAGC 2265
QY 3368 TGGGCTGTGTGACGAACCCCGCTTACGCGGAGCGCTGCGCTTATCGGTAATATC 3427
Db 2264 TGGGCTGTGTGACGAACCCCGCTTACGCGGAGCGCTGCGCTTATCGGTAATATC 2205

QY 3428 GTCTTGAATCCACCCGGTAAAGACAGACTTATCCGCACTGGCAGACGCACTGGTAAACA 3487
 Db 2204 GTCTTGAATCCACCCGGTAAAGACAGACTTATCCGCACTGGCAGACGCACTGGTAAACA 2145
 QY 3488 GGATTAGCAGACGAGGTATGTAGGCGGTGCTACAGAGTTCCTTGAAGTGTGGTCCCTAACT 3547
 Db 2144 GGATTAGCAGACGAGGTATGTAGGCGGTGCTACAGAGTTCCTTGAAGTGTGGTCCCTAACT 2085
 QY 3548 ACGGCTACACTAGAAAGACAGTATTTGTATCTGCGCTCTGCTGAAGCAGTAACTTACCTTG 3607
 Db 2084 ACGGCTACACTAGAAAGACAGTATTTGTATCTGCGCTCTGCTGAAGCAGTAACTTACCTTG 2025
 QY 3608 GAAAAAGAGTGTGAGCTTCTTGAATCCGCAACCAACCGCTGTAGCGGTGTTT 3667
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 QY 3668 TTGTTGCAAGCAGAGATTTAGCGCAGAAAAAGATCTCAAGAAATCTTGTGATCT 3727
 Db 1964 TTGTTGCAAGCAGAGATTTAGCGCAGAAAAAGATCTCAAGAAATCTTGTGATCT 1905
 QY 3728 TTTCTACGCGGTCTGACGCTCAGTGAAGCAAACTCAGCTTAAAGGATTTTGTGATGA 3787
 Db 1904 TTTCTACGCGGTCTGACGCTCAGTGAAGCAAACTCAGCTTAAAGGATTTTGTGATGA 1845
 QY 3788 GATTATCGTCAACCAAGCGGCATCGTCT 3819
 Db 1844 GATTATCAAAAAGATCTTACCTAGATCTTTAAATTAATAAGTTTAAATGA 1785
 QY 3820 3840
 Db 1784 TCTTAAAGTATATAGATTAACCTAGAGCTATGCGAGGCGCTGCGCCGAGCTTGTGCTG 1725
 QY 3841 GCATGATGCGCGATGACCGGCTGTGTTCTGATGCGGAGGATTTGACCTGCGG 3900
 Db 1724 CGAGCCCTGGGCTTCACTCCAACTTGGGGGTGGGTGGGAGAAAGAAACGCGG 1665
 QY 3901 3946
 Db 1664 CGTATTTGGCCCCCAATGGGGTCTCGGTGGGTATGACAGAGTGCAGGCTGGAGACGAA 1605
 QY 3947 TCGGAGAGGATCGA 3961
 Db 1604 CCGCGCTTATGAACAAACCAACCAACCGTGTATCTGTCTTTTATGCGG 1545
 QY 3962 3967
 Db 1544 TCATAGCGCGGTTCTTCCGTAATGTCTCTTCCGTTCAGTTAGCCTCCCTAG 1485
 QY 3968 GGTGGGCGAAGAACTCCAGCATAGATCCCGCTGAGAGTATCCAGCGCGGCTGCC 4027
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 Db 1364 ATGCGAGTTGGGGGTGCTGTGCTGCTGCTTTCGAAATCCCAAGTCCGCTGAAAGAA 1305
 QY 4148 CTCGTCAAGAAAGCGATGAAGGCGATGCGCTGCAATCCGGAAGCGGATACGTTAAG 4207
 Db 1304 CTCGTCAAGAAAGCGATGAAGGCGATGCGCTGCAATCCGGAAGCGGATACGTTAAG 1245
 QY 4208 CACGAGAAAGCGGTCAAGCCATTCGCGCAAGCTCTTCAGCAATATCAAGGTTAGCAA 4267
 Db 1244 CACGAGAAAGCGGTCAAGCCATTCGCGCAAGCTCTTCAGCAATATCAAGGTTAGCAA 1185
 QY 4268 CGCTATGCTGATAGGCGGTCCGCAACCAAGCGCGCAAGTGCATGATCCAGAAA 4327
 Db 1184 CGCTATGCTGATAGGCGGTCCGCAACCAAGCGCGCAAGTGCATGATCCAGAAA 1125

QY 4328 GCGGCATTTTCCACCATGATATTTGGCAGAGGCAATGCGCATGTGGTACAGACAGATC 4387
 Db 1124 GCGGCATTTTCCACCATGATATTTGGCAGAGGCAATGCGCATGTGGTACAGACAGATC 1065
 QY 4388 CTCGCCCTGGGCAATGCGCGCTTGAAGCTTGGCCAAAGTTGCGTGGCGGAGCCCTTG 4447
 Db 1064 CTCGCCCTGGGCAATGCGCGCTTGAAGCTTGGCCAAAGTTGCGTGGCGGAGCCCTTG 1005
 QY 4448 ATGCTCTTGTCCAGATCATCTGTATGACAAAGACCGGCTTCCATCCAGATACGTCG 4507
 Db 1004 ATGCTCTTGTCCAGATCATCTGTATGACAAAGACCGGCTTCCATCCAGATACGTCG 945
 QY 4508 CTCGATGCGATGTTTCTGCTGTGTGCTGATGAGGAGGAGTACCGGATCAAGCTATGAG 4567
 Db 944 CTCGATGCGATGTTTCTGCTGTGTGCTGATGAGGAGGAGTACCGGATCAAGCTATGAG 885
 QY 4568 CCGCGCATTTGATCAGCATGATGATGATATCTTCTCGGAGAGAGCAAGTATGATGAG 4627
 Db 884 CCGCGCATTTGATCAGCATGATGATGATATCTTCTCGGAGAGAGCAAGTATGATGAG 825
 QY 4628 GAGATCTTGGCCCGGCACTTGGCCCAATAGAGCAAGTCCCTTCCGCTTACATGACAAAC 4687
 Db 824 GAGATCTTGGCCCGGCACTTGGCCCAATAGAGCAAGTCCCTTCCGCTTACATGACAAAC 765
 QY 4688 GTGAGCAAGCTGCGCAAGAAAGCGCGGTGTGAGCAGCAGCATAGCGCGCTGCTC 4747
 Db 764 GTGAGCAAGCTGCGCAAGAAAGCGCGGTGTGAGCAGCAGCATAGCGCGCTGCTC 705
 QY 4748 GTCTGCAATTCATTCAGGGGCAACGGAACAGTGTGCTTGAACAATAAGAAACCGGGCGCC 4807
 Db 704 GTCTGCAATTCATTCAGGGGCAACGGAACAGTGTGCTTGAACAATAAGAAACCGGGCGCC 645
 QY 4808 CTGCGCTGACAGCGCGGAAACAGGGGATCAGAGCACCGCATTTCTGTGTGCGCAGTC 4867
 Db 644 CTGCGCTGACAGCGCGGAAACAGGGGATCAGAGCACCGCATTTCTGTGTGCGCAGTC 585
 QY 4868 ATAGCCGAATAGCTCTTCCACCCCAAGGCGCGGAGAACTGCGGCAATCATCTTGTTC 4927
 Db 584 ATAGCCGAATAGCTCTTCCACCCCAAGGCGCGGAGAACTGCGGCAATCATCTTGTTC 525
 QY 4928 AATCATGCAAAAGCATCTCATCTGCTCTTGAATCAGATCTTG 4971
 Db 524 AATCATGCAAAAGCATCTCATCTGCTCTTGAATCAGATCTTG 481

RESULT 7
 US-09-169-425C-7/c
 : Sequence 7, Application US/09169425C
 : Patent No. 6183746
 : GENERAL INFORMATION:
 : APPLICANT: Urban, Robert G.
 : APPLICANT: Chiez, Roman M.
 : APPLICANT: Collins, Edward J.
 : APPLICANT: Hedley, Mary Lynn
 : TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
 : TITLE OF INVENTION: PROTEIN
 : NUMBER OF SEQUENCES: 33
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Fish & Richardson, P.C.
 : STREET: 225 Franklin Street
 : CITY: Boston
 : STATE: MA
 : COUNTRY: US
 : ZIP: 02110-2804
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: Windows95
 : SOFTWARE: FastSeq for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/169,425C
 : FILING DATE: 09-OCT-1998
 : PRIOR APPLICATION DATA:

QY 4688 GTCCAGCAACAGCTGCGCAAGAAAGCCCGTGTGCGCAGCCAGATAGCCCGCTGCTC 4747
 Db 764 GTCCAGCAACAGCTGCGCAAGAAAGCCCGTGTGCGCAGCCAGATAGCCCGCTGCTC 705
 QY 4748 GTCCGCGATTCATTCAGGGCAAGCGAGAGGTGGTCTTGAACAAAAGAACCGGGCGCC 4807
 Db 704 GTCTTGCAATTCATTCAGGGCAAGCGAGAGGTGGTCTTGAACAAAAGAACCGGGCGCC 645
 QY 4808 CTGGCTGACAGCCGGAACAGCGGGGCGATCAGAGAGCGGATGTCCTTTGGCCCACTC 4867
 Db 644 CTGGCTGACAGCCGGAACAGCGGGGCGATCAGAGAGCGGATGTCCTTTGGCCCACTC 585
 QY 4868 ATAGCCGAAATAGCTCTTCACCCAGCGGGCGGAACCTGCGTGCATTCCTTTGTC 4927
 Db 584 ATAGCCGAAATAGCTCTTCACCCAGCGGGCGGAACCTGCGTGCATTCCTTTGTC 525
 QY 4928 AATCATGCGAAACGATCTCTCATCTCTCTTTGATCAGATCTTG 4971
 Db 524 AATCATGCGAAACGATCTCTCATCTCTCTTTGATCAGATCTTG 481

RESULT 8

US-09-759-960-7/C
 Sequence 7, Application US/09759960
 Patent No. 6582704
 GENERAL INFORMATION:
 APPLICANT: Urban, Robert G.
 APPLICANT: Chicz, Roman M.
 APPLICANT: Collins, Edward J.
 APPLICANT: Hedley, Mary Lynn
 TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/759,960
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/169,425
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 08191/004002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-5070
 TELEFAX: 617-543-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4665 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-09-759-960-7

Query Match 29 7%; Score 1571.6; DB 3; Length 4665;
 Best Local Similarity 86.3%; Pred. No. 0;
 Matches 1850; Conservative 0; Mismatches 114; Indels 180; Gaps 3;

QY 3008 ACTCAAAAGCGGTAAATACGGTTATCCACAGATCAGGGGATTAACGACAGAAAGAAATGT 3067
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 QY 3068 GAGCAAAAGCGCACAAAGGCGCAGAAACCGTAATAAGGCGCGTGTGCGCTTTTCC 3127
 Db 2564 GAGCAAAAGGCGCACAAAGGCGCAGAAACCGTAATAAGGCGCGCTGTGCGCTTTTCC 2505
 QY 3128 AATAGGCTCCCGCCCGCTGACAGATCACAATAATTCAGCTCAAGTACAGGTGCGCA 3187
 Db 2504 AATAGGCTCCCGCCCGCTGACAGATCACAATAATTCAGCTCAAGTACAGGTGCGCA 2445
 QY 3188 ACCGCAAGAGACTTAAGATACAGAGCGTTTCCCGTGAAGGCTCCCTGTGCGCTC 3247
 Db 2444 ACCGCAAGAGACTTAAGATACAGAGCGTTTCCCGTGAAGGCTCCCTGTGCGCTC 2385
 QY 3248 CTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCCTTCGGGAAGCGTG 3307
 Db 2384 CTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCCTTCGGGAAGCGTG 2325
 QY 3308 CGCTTTCTCATAGTCAAGCTGTAGGTATCTCAGTTGGGTAGGTGCTTCCCAAGC 3367
 Db 2324 CGCTTTCTCATAGTCAAGCTGTAGGTATCTCAGTTGGGTAGGTGCTTCCCAAGC 2265
 QY 3368 TGAGCTGTGACAGAAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGTAATATC 3427
 Db 2264 TGAGCTGTGACAGAAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGTAATATC 2205
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 QY 3488 GATTTACAGAGGAGGTATGTAGGCGGTCTACAGATTCTTGAAGTGTGCTTAAT 3547
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 QY 3548 ACGGCTACACTAAGAAAGATTTTGTATTCGCGCTGCTGAACCGGTAATCTTG 3607
 Db 2084 ACGGCTACACTAAGAAAGATTTTGTATTCGCGCTGCTGAACCGGTAATCTTG 2025
 QY 3608 GAAAGAGTTGTAGTCTTGTATCCGCAAAACCAACCGCTGTAGCGGTGTTT 3667
 Db 2024 GAAAGAGTTGTAGTCTTGTATCCGCAAAACCAACCGCTGTAGCGGTGTTT 1965
 QY 3668 TTGTTTTCAGACGACGATTAACGCGCAAAAGAAAGATTCAGAGATCTTGAATCT 3727
 Db 1964 TTGTTTTCAGACGACGATTAACGCGCAAAAGAAAGATTCAGAGATCTTGAATCT 1905
 QY 3728 TTTCTACGCGGCTGACGCTCAGTGAAGAAACTCAGTTAAGGATTTTGTATGA 3787
 Db 1904 TTTCTACGCGGCTGACGCTCAGTGAAGAAACTCAGTTAAGGATTTTGTATGA 1845
 QY 3788 GATTATCTGACCAAAAGCGGCGATGCTCTT----- 3819
 Db 1844 GATTATCAAAAGAGATCTTACCTAGATCTTTTAATTAATAAGTTTAAATCAA 1785
 QY 3820 -----CCCACTCTGCAAGTTGGGG 3840
 Db 1784 TCTAAGATATATGAGTAACCTGAGGCTATGCGAGGCGCTGCGCGCCAGCTGTGCTG 1725
 QY 3841 GCATGATGCGCGGATAGCGGCTGTGTTCTGTGATGCGACGATTTGCACTGCGG 3900
 Db 1724 CGAGCCCTGGCTTCACTCGAACTTTGGGGGTGGGGTGGGAAAGAAACGCGGG 1665
 QY 3901 -----TAGAACTCCGCAAGTGTCTCAGCTCAGCGACGCTGAACCAAC 3946
 Db 1664 CGTATTGGCCCCCAATGGGGGTCTGATGGGGTATCGACAGTGTCCAGCCCTGGGACGAA 1605
 QY 3947 TCGCGAGGGGATGA----- 3961
 Db 1604 CCGCGGTTTATGAACAAACCAACCGGCTTATTTCTGTCTTTTATTCGCG 1545
 QY 3962 -----GCCCG 3967

Db 2255 TGGGCTGTGTACAGCAACCCCGCTTTCAGCCGACCGCTGCGCTTATCCGTAACATATC 2314
 Qy 3428 GTCTTGAAGTCCACCCCGCTTAAAGACAGCATTAATGCGCACTGCGACGACCACTGTAACA 3487
 Db 2315 GTCTTGAAGTCCACCCCGCTTAAAGACAGCATTAATGCGCACTGCGACGACCACTGTAACA 2374
 Qy 3488 GGAATTAGCAGACGAGGATATGAGCGGTGCTACAGAGTTCTTGAAGTGTGACTTAAT 3547
 Db 2275 GGAATTAGCAGACGAGGATATGAGCGGTGCTACAGAGTTCTTGAAGTGTGACTTAAT 2434
 Qy 3548 ACCGCTACACTAGAAAGAACATATTTGGTATCTGCGCTCTGTGAGCCAGTTACTTTCG 3607
 Db 2435 ACCGCTACACTAGAAAGAACATATTTGGTATCTGCGCTCTGTGAGCCAGTTACTTTCG 2494
 Qy 3608 GAAAAAGATTGTGAGCTCTTGAATCCGCGCAACCAACACCGCTGTGAGCGGTGTTT 3667
 Db 2495 GAAAAAGATTGTGAGCTCTTGAATCCGCGCAACCAACACCGCTGTGAGCGGTGTTT 2554
 Qy 3668 TTGTTTGCACACAGATTAACGCGCAGAAAAAGATCTCAAGAAATCTTGTGATCT 3727
 Db 2555 TTGTTTGCACACAGATTAACGCGCAGAAAAAGATCTCAAGAAATCTTGTGATCT 2614
 Qy 3728 TTTCTACGGGCTCTGACGCTCACTGAGAAAGAACTCACTTAAGGATTTTGTGATGA 3787
 Db 2615 TTTCTACGGGCTCTGACGCTCACTGAGAAAGAACTCACTTAAGGATTTTGTGATGA 2674
 Qy 3788 GATTATGTGACCAAGAGCGGCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3819
 Db 2675 GATTATGTGACCAAGAGCGGCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2734
 Qy 3820 TCTAAAGTATATATAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 3840
 Db 2735 TCTAAAGTATATATAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 2794
 Qy 3841 GCATGATGCGCGGATGAGCGCTGCTGTTTCTGATGCGGACGATTTGCACTGCGG 3900
 Db 2795 CGAGCCCTGGGCTCTTCAACCGCACTTGGGGGTGGGGAAGAAAGAAAGAAAGAAAGAAAG 2854
 Qy 3901 TAAAGCTCCGCGAGGTGCTCAAGCTTCAAGCAGTCAAGCAGTCAAGCAGTCAAGCAGTCAAG 3946
 Db 2855 CGTATGTCCTCCCAATGAGGAGTCTGCTGAGGATATGACAGAGTGCACGCTGAGGACCGAA 2914
 Qy 3947 TCGGAGGGGATCGA----- 3961
 Db 2915 CCGCGCTTTATGAACAAAGCAACCAACCGTCCGTTTATCTGCTTTTATTTGCGG 2974
 Qy 3962 TCAATAGCGGAGTCTCTTCCGATATGTCCTTCCGTTTCAAGTTAGCTCCCGCTAG 3034
 Db 2975 TCAATAGCGGAGTCTCTTCCGATATGTCCTTCCGTTTCAAGTTAGCTCCCGCTAG 3034
 Qy 3968 GGTGGGGAAGAACTCCAGCATGAGATCCCGCGCTGAGGATATCAAGCGCGCTGCC 4027
 Db 3035 GGTGGGGAAGAACTCCAGCATGAGATCCCGCGCTGAGGATATCAAGCGCGCTGCC 3094
 Qy 4028 GAAAAAGATTTCGAGCCCACTTCAATAGAAAGGCGGTGGAATTCGAATCTGCTG 4087
 Db 3095 GAAAAAGATTTCGAGCCCACTTCAATAGAAAGGCGGTGGAATTCGAATCTGCTG 3154
 Qy 4088 ATGCGAGTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4147
 Db 3155 ATGCGAGTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3214
 Qy 4148 CTGCTCAAGAAAGGATGAAAGGCGATGCGGATTCGAGAGCGCGGATACCGTAAAG 4207
 Db 3215 CTGCTCAAGAAAGGATGAAAGGCGATGCGGATTCGAGAGCGCGGATACCGTAAAG 3274
 Qy 4208 CACGAGAAAGCGGTCAAGCTTTCGCGCAAGCTTTCAGCAATATCAAGGATAGCA 4267
 Db 3275 CACGAGAAAGCGGTCAAGCTTTCGCGCAAGCTTTCAGCAATATCAAGGATAGCA 3334
 Qy 4268 CGCTATGCTGATAGGCTGCGGACACCGCGGCAAGTGTGATTCAGAA 4327

Db 3335 CGTATGCTGTATGAGCGGTCCGCAACCAAGCGGCAAGTGTGATTCAGAA 3394
 Qy 4328 GCGGCAATTTTCCACATGATATTCGGAACAGGATTCGCAATGAGTCAAGAGATC 4387
 Db 3395 GCGGCAATTTTCCACATGATATTCGGAACAGGATTCGCAATGAGTCAAGAGATC 3454
 Qy 4388 CTCGCCGTGCGGCAATGCGGCTTGAAGCTGGCAACAGTTGCGGCTGGCGGAGCCCTG 4447
 Db 3455 CTCGCCGTGCGGCAATGCGGCTTGAAGCTGGCAACAGTTGCGGCTGGCGGAGCCCTG 3514
 Qy 4448 ATGCTCTTGTGCATGATCATCTGATGACAAAGACCGCTTTCATCCGATGATGCTCG 4507
 Db 3515 ATGCTCTTGTGCATGATCATCTGATGACAAAGACCGCTTTCATCCGATGATGCTCG 3574
 Qy 4508 CTGATGAGATGTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4567
 Db 3575 CTGATGAGATGTTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3634
 Qy 4568 CCGCGCATTTGCATCAGCATGATGATTACTTTCGCGAGAGCAAGGTGATGACAG 4627
 Db 3635 CCGCGCATTTGCATCAGCATGATGATTACTTTCGCGAGAGCAAGGTGATGACAG 3694
 Qy 4628 GAGATCTGCTCCCGGCACTTCCGCAATAGCAGCAGTCCCTTCCGCTTCACTGACAC 4687
 Db 3695 GAGATCTGCTCCCGGCACTTCCGCAATAGCAGCAGTCCCTTCCGCTTCACTGACAC 3754
 Qy 4688 GTGAGCAACAGTCTGCGAAGAACGCGCTGCTGCGCAAGCAGATGACGCGCTGCTC 4747
 Db 3755 GTGAGCAACAGTCTGCGAAGAACGCGCTGCTGCGCAAGCAGATGACGCGCTGCTC 3814
 Qy 4748 GTCTGAGTTCATTCAGAGGACCGGACAGGCTGCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAG 4807
 Db 3815 GTCTGAGTTCATTCAGAGGACCGGACAGGCTGCTTGAAGAAAGAAAGAAAGAAAGAAAGAAAG 3874
 Qy 4808 CTGCGTGAACCGGAAACAGCGGCGATCAGAGCAGCAGTCTGTTGTGCTGCAATC 4867
 Db 3875 CTGCGTGAACCGGAAACAGCGGCGATCAGAGCAGCAGTCTGTTGTGCTGCAATC 3934
 Qy 4868 ATAGCCGAATGAGCTCTTCAACCCAGGCGCGGAGAACTGCGTGCATCATTTGTTTC 4927
 Db 3935 ATAGCCGAATGAGCTCTTCAACCCAGGCGCGGAGAACTGCGTGCATCATTTGTTTC 3994
 Qy 4928 AATCATGCAAGAGATCTCATCTGCTCTTGAATGATCTTG 4971
 Db 3995 AATCATGCAAGAGATCTCATCTGCTCTTGAATGATCTTG 4038

RESULT 10
 US-09-533-220A-4/C
 ; Sequence 4, Application US/09533220A
 ; Patent No. 6406908
 ; GENERAL INFORMATION:
 ; APPLICANT: McInyre, Peter
 ; APPLICANT: James, Iain Fraser
 ; TITLE OF INVENTION: Human Vanilloid Receptor
 ; FILE REFERENCE: 4-30875A
 ; CURRENT APPLICATION NUMBER: US/09/533,220A
 ; PRIORITY FILING DATE: 2000-03-23
 ; PRIOR FILING DATE: 1999-03-26
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 1.30
 ; SEQ ID NO 4
 ; LENGTH: 4886
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-533-220A-4

Query Match 29.7%; Score 1570; DB 3; Length 4886;
 Best Local Similarity 86.2%; Pred. No. 0;
 Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

Qy 3008 ACTCAAGGCGGATATGAGGATATTCACAGAAATCAGGGGATTAACGAGAAAGAAATGT 3067

Db 4295 AATGCAATGGCGGTAATACGTTATCCACAGATACGGGATTAAGCAGAAAGACATGT 4236
QY 3068 GAGCAAAAGCCAGCAAAAGCCAGGAACCGTAAAGAGCCGGCTGCTGCTTTTCC 3127
Db 4235 GAGCAAAAGCCAGCAAAAGCCAGGAACCGTAAAGAGCCGGCTGCTGCTTTTCC 4176
QY 3128 ATAGGCTCCGCCCCCGACGAGCATCAAAAAATGACCTCAAGTCAGAGGTGGGAA 3187
Db 4175 ATAGGCTCCGCCCCCGACGAGCATCAAAAAATGACCTCAAGTCAGAGGTGGGAA 4116
QY 3188 ACCGCAAGCACTATAAGATACCAAGCGTTCCTCCCTGGAAGCTCCCTGCGCTCTC 3247
Db 4115 ACCGCAAGCACTATAAGATACCAAGCGTTCCTCCCTGGAAGCTCCCTGCGCTCTC 4056
QY 3248 CTGTTCGCAACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTGGGAAAGCGTGG 3307
Db 4055 CTGTTCGCAACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTGGGAAAGCGTGG 3996
QY 3308 CGCTTCTCATAGCTACGCTGATAGTATCTCAGTTGGGTGATGGTTCGCTCCAGC 3367
Db 3995 CGCTTCTCATAGCTACGCTGATAGTATCTCAGTTGGGTGATGGTTCGCTCCAGC 3936
QY 3368 TGGGCTGTGACGAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGTTAATCTATC 3427
Db 3935 TGGGCTGTGACGAACCCCGCTTCAGCCCGACCGCTGCGCTTATCCGTTAATCTATC 3876
QY 3428 GTCTTGAGTCCAAACCCGGTAAAGACAGACTTATGCGCATGCGACGCCATCTGTAA 3487
Db 3875 GTCTTGAGTCCAAACCCGGTAAAGACAGACTTATGCGCATGCGACGCCATCTGTAA 3816
QY 3488 GGATTACAGAGGATATGAGCGGTGACAGAGTCTTGAAGTGGGCTTAAT 3547
Db 3815 GGATTACAGAGGATATGAGCGGTGACAGAGTCTTGAAGTGGGCTTAAT 3756
QY 3548 ACCGCTACACTAGAAAGACAGTATTTGTGATCTGCGCTGCTGAGACCATCTTCC 3607
Db 3755 ACCGCTACACTAGAAAGACAGTATTTGTGATCTGCGCTGCTGAGACCATCTTCC 3696
QY 3608 GAAAAAGAGTGGTGAAGCTCTTGAATCCGGCAAAACAACCGCTGTAGCGGTGTTTTT 3667
Db 3695 GAAAAAGAGTGGTGAAGCTCTTGAATCCGGCAAAACAACCGCTGTAGCGGTGTTTTT 3636
QY 3668 TTGTTTCAAGCAGCAGATTAACGCGCAGAAAAAGAGTCTCAAGAGATCTTGTATCT 3727
Db 3635 TTGTTTCAAGCAGCAGATTAACGCGCAGAAAAAGAGTCTCAAGAGATCTTGTATCT 3576
QY 3728 TTCTACGGGGTCTGACGCTCAAGTGAACGAAAACTCAGTTAAGGATTTTGTCTATGA 3787
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QY 3788 GATTATGCTGACCAAAAGCGGCTCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3819
Db 3515 GATTATCAAAAAAGATCTTCACTTGAATCTTTTAAATGAAGTTTAAATCAA 3456
QY 3820 -----CCCACTCTGATGTTCCGGG 3840
Db 3455 TCTTAAATATATATGATTAACCTGAGCTATGCGAGGCTCGCGCCCAAGCTTGGCTG 3396
QY 3841 GCATGATGCGCGGATAGCCGCTGCTGCTTCTGATGCGCAGATTTGCACTGCGG 3900
Db 3395 CGAGCCCTGGGCTTCAACCGAACTTGGGGGGTGGGGTGGGAAAGAAAGAAACGCGGG 3336
QY 3901 -----TAAAGCTCCGCGAGTGTCTCAGCTCAGGCAAGCTGAAACCAAC 3946
Db 3335 CGATATGCCCCCAATGAGGTCTCGGTGGGTATGACAGAGTGCACCCCTGGGACCGAA 3276
QY 3947 TCGGAGAGGATCGA----- 3961
Db 3275 CCGCGCTTATTAAGAAAGAACCAACCAACCGGTGCTTATTTCTGCTTTTATTTGCGG 3216
QY 3962 -----GCCCGG 3967

Db 3215 TCATAGCGGGGTTCTTCCTCCGATATTGTCTCTCCGTGTTCAAGTAACTCCCTAG 3156
QY 3968 GGTGGCGAAAGAACTCCAGCATGAGATCCCGCGCTGAGAGATCATTCAGCCGGCTCCC 4027
Db 3155 GGTGGCGAAAGAACTCCAGCATGAGATCCCGCGCTGAGAGATCATTCAGCCGGCTCCC 3096
QY 4028 GAAAAAGATTCGGAAGCCCAACTTTCAATAGAAAGCGCGGTGAATGAAATCTCGTG 4087
Db 3095 GAAAAAGATTCGGAAGCCCAACTTTCAATAGAAAGCGCGGTGAATGAAATCTCGTG 3036
QY 4088 ATGACAGTTGGGCGTTCGCTTGGTTCGATCTTCAAGCCCAAGTCCGCTCAGAAAG 4147
Db 3035 ATGACAGTTGGGCGTTCGCTTGGTTCGATCTTCAAGCCCAAGTCCGCTCAGAAAG 2976
QY 4148 CTGTCAAGAGCCGATTAAGGCGATGGGCTGCGCAATGGGAGCGGCGATCCGTTAAG 4207
Db 2975 CTGTCAAGAGCCGATTAAGGCGATGGGCTGCGCAATGGGAGCGGCGATCCGTTAAG 2916
QY 4208 CACGAGAAAGCGGTGACCCATTCGCGCGCAAGCTTTCAAGCAATATCAAGGTTAGCAA 4267
Db 2915 CACGAGAAAGCGGTGACCCATTCGCGCGCAAGCTTTCAAGCAATATCAAGGTTAGCAA 2856
QY 4268 CGCTATGCTCTGATAGCGGTTCGCGCAACCCAGCCGCGCAAGTGCATGATATCAGAAA 4327
Db 2855 CGCTATGCTCTGATAGCGGTTCGCGCAACCCAGCCGCGCAAGTGCATGATATCAGAAA 2796
QY 4328 GCGGCAATTTTCCACATGATATTCGCAAGAGGATGCCATGGGTACAGCAGATC 4387
Db 2795 GCGGCAATTTTCCACATGATATTCGCAAGAGGATGCCATGGGTACAGCAGATC 2736
QY 4388 CTCGCCGTGGGATGCGGCTTGAGCTGCGCAACAGTTGGCTGGCGGCGAGCCCTG 4447
Db 2735 CTCGCCGTGGGATGCGGCTTGAGCTGCGCAACAGTTGGCTGGCGGCGAGCCCTG 2676
QY 4448 ATGCTCTTGTCCAGATCATCTGATGCAAGAACCGGCTTCCATCCAGATACGTCTCG 4507
Db 2675 ATGCTCTTGTCCAGATCATCTGATGCAAGAACCGGCTTCCATCCAGATACGTCTCG 2616
QY 4508 CTCGATGCCATGTTGGTGTGTCGATAGGGGAGGTAGCCGATCAAGGCTATGCA 4567
Db 2615 CTCGATGCCATGTTGGTGTGTCGATAGGGGAGGTAGCCGATCAAGGCTATGCA 2556
QY 4568 CCGCGCATTTGATCAGCATGATGATATCTTCTCGGAGAGCAAGGTGATGACAG 4627
Db 2555 CCGCGCATTTGATCAGCATGATGATATCTTCTCGGAGAGCAAGGTGATGACAG 2496
QY 4628 GAGATCTGCCCCGGCACTTCCGCAATAGCAGCGATCTTCCGCTTCAATGCAAC 4687
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QY 4688 GTGAGACACAGCTGGCAAGAAAGCGCGGTGCGCAGCACGATAGCGGCTGCTC 4747
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QY 4748 GTCTGCACTTCAATGAGGCAACCGGACAGTGTGATCTTGAACAAAAAGAACCGGGCGCC 4807
Db 2375 GTCTGCACTTCAATGAGGCAACCGGACAGTGTGATCTTGAACAAAAAGAACCGGGCGCC 2216
QY 4808 CTGCGCTGACAGCCGGAACAGCGCGGATCAAGAGCAGCGATTTGCTGTTGCGCAAGTC 4867
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QY 4868 ATAGCCGAATAGCTCTCCACCCCAAGCGGCGGAGAACTGCGTGCATTCATCTTGTTC 4927
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QY 4928 AATCATGCAAAAGATCTCATCTCTCTCTTGTATGATCTTGG 4971
Db 2195 AATCATGCAAAAGATCTCATCTCTCTTGTATGATCTTGG 2152

Sequence 4, Application US/10128853
Patent No. 6887978
GENERAL INFORMATION:
APPLICANT: Mcintyre, Peter
APPLICANT: James, Iain Fraser
TITLE OF INVENTION: Human Vanilloid Receptor
FILE REFERENCE: 4-30875A
CURRENT APPLICATION NUMBER: US/10/128, 853
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US/09/533,220
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 1.30
SEQ ID NO 4
LENGTH: 4886
TYPE: DNA
ORGANISM: Homo sapiens
US-10-128-853-4

Query Match 29.7%; Score 1570; DB 3; Length 4886;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

QY 3008 ACTCAAGCGGATATACGGTTATCCAGATCAGGGGATTAACGAGAAAGACATGT 3067
DB 4295 AATGCAATGGGGATATACGGTTATCCACAGATACGGGGATTAACGAGAAAGACATGT 4236
QY 3068 GAGCAAAAGCCAGCAAAAGCCAGAAACCGTAAAGAGCCGCTGCTGCGCTTTTCC 3127
DB 4235 GACCAAAAGCCAGCAAAAGCCAGAAACCGTAAAGAGCCGCTGCTGCGCTTTTCC 4176
QY 3128 ATAGGCTCCGCGCCCGCTGAGAGATCAAAAAATCAGCTCAAGTCAAGAGTGGGAA 3187
DB 4175 ATAGGCTCCGCGCCCGCTGAGAGATCAAAAAATCAGCTCAAGTCAAGAGTGGGAA 4116
QY 3188 ACCGCAAGAGCTATAAGATATACAGAGCGTTTCCCGCTGAGAGTCCCTGCTGCTC 3247
DB 4115 ACCGCAAGAGCTATAAGATATACAGAGCGTTTCCCGCTGAGAGTCCCTGCTGCTC 4056
QY 3248 CTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCCGGAAGCGTG 3307
DB 4055 CTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCCGGAAGCGTG 3396
QY 3308 CGCTTTCTATAGCTACAGCTGTAAGTATCTCAATTGCGTGAAGTGTTCCTCCAGC 3367
DB 3395 CGCTTTCTATAGCTACAGCTGTAAGTATCTCAATTGCGTGAAGTGTTCCTCCAGC 3336
QY 3368 TGGGCTGTGTCAGAAACCCCGCTTACGCGCGGCTGCGCTTATCCGATACATC 3427
DB 3393 TGGGCTGTGTCAGAAACCCCGCTTACGCGCGGCTGCGCTTATCCGATACATC 3876
QY 3428 GTCTTGAAGTCAACCCCGGTAAGACAGACTTATCGCACTGCGAGCACTGTAAACA 3487
DB 3875 GTCTTGAAGTCAACCCCGGTAAGACAGACTTATCGCACTGCGAGCACTGTAAACA 3816
QY 3488 GATTAGCAGAGGAGGTATGAGGCGGTCTACAGATTCTTGAAGTGTGCTTAAT 3547
DB 3815 GATTAGCAGAGGAGGTATGAGGCGGTCTACAGATTCTTGAAGTGTGCTTAAT 3756
QY 3548 ACGGCTACATAGAGAAAGATATTTGGTATCTGCGCTGCGAGAGCCAGTTACCTTCG 3607
DB 3755 ACGGCTACATAGAGAAAGATATTTGGTATCTGCGCTGCGAGAGCCAGTTACCTTCG 3696
QY 3608 GAAAAAGATTGTAAGTCTTGAATCCGCAAAACCAACCGCTGTAAGCGGTGTTTTT 3667
DB 3695 GAAAAAGATTGTAAGTCTTGAATCCGCAAAACCAACCGCTGTAAGCGGTGTTTTT 3636
QY 3668 TTGTTTGAAGCAGCATTAACGCGCAAAAAAGGATCTCAAGAAAGATCTTTGATCT 3727
DB 3635 TTGTTTGAAGCAGCATTAACGCGCAAAAAAGGATCTCAAGAAAGATCTTTGATCT 3576

QY 3728 TTCTCAAGGAGTCTGACGCTCAGTGAACGAAACCTACCGTTAAGGATTTTGTCAATGA 3787
DB 3575 TTCTCAAGGAGTCTGACGCTCAGTGAACGAAACCTACCGTTAAGGATTTTGTCAATGA 3516
QY 3788 GATTATCTGACCAAAAGCCGCAATCGTCTT----- 3819
DB 3515 GATTATCAAAAGAGATCTTCACTAGATCTTTAAATTAATAAGATTTTAATCA 3456
QY 3820 -----CCCACTCTGCAAGTTCGGG 3840
DB 3455 TCTAAAGTATATATAGTAACTGAGGCTATGCAAGGCTGCGCCGCAAGTTCGCTG 3396
QY 3841 GCATGATGCGCGGATGACCGCTGCTGTTTCTGATGCGCAACGATTTGCACTGCGG 3900
DB 3395 CGAGCCCTGGGCTTTCACCCGAACTTGGGGGTGGGGTGGGAAAGAAAGAACGCGG 3336
QY 3901 -----TAGAACTCCGCGAGGTGCTTCAGCCTCAAGCAGCACTGAACCAAC 3946
DB 3335 CGTATGCCCCCAATGGGGTCTCGTGGGGTATCGACAGATGCAACCTGGAACGAA 3276
QY 3947 TCCGAGGGGATGCA----- 3961
DB 3275 CCGCGGTTATGAACAAACGACCACACCGTGCCTTTATTTCTGTTTATTCGCG 3216
QY 3962 -----GCCCG 3967
DB 3215 TCATAGCGGGTCTTCCGGTATGTCCTTCCTCCGTTTCAAGTACCTCCCTAG 3156
QY 3968 GGTGGGCAAGAACTCCAGCATAGATCCCGCGCTGAGAGATCATCAGCCGCGTCC 4027
DB 3155 GGTGGGCAAGAACTCCAGCATAGATCCCGCGCTGAGAGATCATCAGCCGCGTCC 3096
QY 4028 GAAAAAGATTTCCGAAGCCCACTTTCAATAGAAGGGGGGTGAATTCGAAATCTGTG 4087
DB 3095 GAAAAAGATTTCCGAAGCCCACTTTCAATAGAAGGGGGGTGAATTCGAAATCTGTG 3036
QY 4088 ATGCAAGTGTGGGCGTCCGCTTGTGCTATTCGAAACCCAGAGTCCGCTCGAAGAA 4147
DB 3035 ATGCAAGTGTGGGCGTCCGCTTGTGCTATTCGAAACCCAGAGTCCGCTCGAAGAA 2976
QY 4148 CTGTCAGAAAGCGATAGAAAGCGATGCGCTCGAATCGGAGCGCGCATACGTTAAG 4207
DB 2975 CTGTCAGAAAGCGATAGAAAGCGATGCGCTCGAATCGGAGCGCGCATACGTTAAG 2916
QY 4208 CAGAGAAAGCGGTCAAGCCATTCGCGCCCAAGCTTTCAAGCAATATCAGGGTACGCA 4267
DB 2915 CAGAGAAAGCGGTCAAGCCATTCGCGCCCAAGCTTTCAAGCAATATCAGGGTACGCA 2856
QY 4268 CGCTATGCTCTGATAGCGGTCCGCAACCCAGCCGCGCAAGTTCAGTAATCAGAAAA 4327
DB 2855 CGCTATGCTCTGATAGCGGTCCGCAACCCAGCCGCGCAAGTTCAGTAATCAGAAAA 2796
QY 4328 GCGGCAATTTTCCACATGATATTTCCGCAAGCAGGATCGCATGGGTCAAGAGATC 4387
DB 2795 GCGGCAATTTTCCACATGATATTTCCGCAAGCAGGATCGCATGGGTCAAGAGATC 2736
QY 4388 CTGCGGCTGGGATGCGCGCTTGAAGCTGCGAAAGATTGCGGTGCGCGAGCCCTG 4447
DB 2735 CTGCGGCTGGGATGCGCGCTTGAAGCTGCGAAAGATTGCGGTGCGCGAGCCCTG 2676
QY 4448 ATGCTCTGCTCAGATCAATCCGATCGAACAGCGGCTTCAATCGAGTATGCTGCTG 4507
DB 2675 ATGCTCTGCTCAGATCAATCCGATCGAACAGCGGCTTCAATCGAGTATGCTGCTG 2616
QY 4508 CTGATGCAATGTTTCTGCTGCTGCTGCTGATGAGGAGGATGAGCCGATGCAAGCTATGCA 4567
DB 2615 CTGATGCAATGTTTCTGCTGCTGCTGCTGATGAGGAGGATGAGCCGATGCAAGCTATGCA 2556
QY 4568 CCGCGCATTTGCAATGCAAGCATGATGATCTTTCTGCGAGGAGCAAGTGAATGACAG 4627
DB 2555 CCGCGCATTTGCAATGCAAGCATGATGATCTTTCTGCGAGGAGCAAGTGAATGACAG 2496
QY 4628 GAGATCTGCGCGGCACTTCCGCAATGAGCAGTCCCTTCCGCTTCAAGTCAAC 4687

Db 2495 GAGATCTGCCCCGGGCACTTCCGCAATGACACGAGTCCCTTCCGCTTCATGACAC 2436
Qy 4688 GTGAGCACTGTCGCGAAGAAAGCCCGTGTGGCCAGCAGATACCGCGCTGCTC 4747
Db 2435 GTGAGCACTGTCGCGAAGAAAGCCCGTGTGGCCAGCAGATACCGCGCTGCTC 2376
Qy 4748 GTGAGCACTGTCGCGAAGAAAGCCCGTGTGGCCAGCAGATACCGCGCTGCTC 4807
Db 2375 GTGAGCACTGTCGCGAAGAAAGCCCGTGTGGCCAGCAGATACCGCGCTGCTC 2316
Qy 4808 GTGAGCACTGTCGCGAAGAAAGCCCGTGTGGCCAGCAGATACCGCGCTGCTC 4867
Db 2315 GTGAGCACTGTCGCGAAGAAAGCCCGTGTGGCCAGCAGATACCGCGCTGCTC 2256
Qy 4868 ATGAGCGAATGAGCTCTCCACCCAGCGCGCGAAGAACTGCTGATCATCTTTGTC 4927
Db 2255 ATGAGCGAATGAGCTCTCCACCCAGCGCGCGAAGAACTGCTGATCATCTTTGTC 2196
Qy 4928 AATCATGCGAAGATCTGATCTGCTGATCATCTTTG 4971
Db 2195 AATCATGCGAAGATCTGATCTGCTGATCATCTTTG 2152

RESULT 12

US-08-751-767A-7/c
Sequence 7, Application US/08751767A

Patent No. 5994104

GENERAL INFORMATION:

APPLICANT: ANDERSON, ROBERT J.

APPLICANT: GRANT, HUGH

APPLICANT: MACDONALD, IAN D.

TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYTE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/751,767A

FILING DATE: 08-NOV-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 117-221

TELECOMMUNICATION INFORMATION:

TELEPHONE: 7038164091

TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 6139 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 3222..4841

US-08-751-767A-7

Query Match 29.7%; Score 1570; DB 2; Length 6139;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

Qy 3008 ACTCAAGGCGGTAATAGGTTATCCAGATCAGGGGATTAACGAGGAAGAAACATGT 3067
Db 2624 AATGATGCGGTAATAGGTTATCCAGATCAGGGGATTAACGAGGAAGAAACATGT 2565
Qy 3068 GAGCAAAAGCCAGCAAAAGCCAGAAACCGTAAAAAGGCGGCTTGCAGGTTTTCC 3127
Db 2564 GAGCAAAAGCCAGCAAAAGCCAGAAACCGTAAAAAGGCGGCTTGCAGGTTTTCC 2505
Qy 3128 ATAGGCTCCGCCCCCTGACAGCATCACAATAATGACGCTCAAGTCAAGAGTCCGA 3187
Db 2504 ATAGGCTCCGCCCCCTGACAGCATCACAATAATGACGCTCAAGTCAAGAGTCCGA 2445
Qy 3188 ACCCGACAGACTAATTAAGATACAGGCGTTTCCCTGGAAGTCCCTGCGCTCTC 3247
Db 2444 ACCCGACAGACTAATTAAGATACAGGCGTTTCCCTGGAAGTCCCTGCGCTCTC 2385
Qy 3248 GTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTGGGAAGCTGG 3307
Db 2384 GTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTGGGAAGCTGG 2325
Qy 3308 CGCTTTCTATAGCTCAGCGCTGATGATCTCAAGTTCGATGATGATGATGATGATG 3367
Db 2324 CGCTTTCTATAGCTCAGCGCTGATGATCTCAAGTTCGATGATGATGATGATGATG 2265
Qy 3368 TGAGGCTGTGACAGAAACCCCGCTTACGCGCCGACCGCGCTTATCCGTTAACTATC 3427
Db 2264 TGAGGCTGTGACAGAAACCCCGCTTACGCGCCGACCGCGCTTATCCGTTAACTATC 2205
Qy 3428 GTCTTGAAGTCAACCCCGGTAAAGACAGACTTATGCGCATGCGACAGCACTGTGTACA 3487
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Db 2144 GGAATTAGCAGACGAGATATGAGGCGGTCACAGAGTCTTGAAGTGTGGGCTTAAT 2085
Qy 3548 ACGGCTACACTAGAAAGAAACAGATTTGATCTGCGCTGCGAAGCCAGTTACCTTGC 3607
Db 2084 ACGGCTACACTAGAAAGAAACAGATTTGATCTGCGCTGCGAAGCCAGTTACCTTGC 2025
Qy 3608 GAAAAAGATTGATGATCTTGAATCCGCAAAACCAACCGCTGTGAGCGGTTTTT 3667
Db 2024 GAAAAAGATTGATGATCTTGAATCCGCAAAACCAACCGCTGTGAGCGGTTTTT 1965
Qy 3668 TTGTTTTCAGAGAGAGATTAAGCGGAGAAAAAGATCTCAAGAGATCTTGAATCT 3727
Db 1964 TTGTTTTCAGAGAGAGATTAAGCGGAGAAAAAGATCTCAAGAGATCTTGAATCT 1905
Qy 3728 TTTTACGAGGATCTGACGCTCAGTGGAAAGAAACTCAGCTTAAGGATTTTGATGTA 3787
Db 1904 TTTTACGAGGATCTGACGCTCAGTGGAAAGAAACTCAGCTTAAGGATTTTGATGTA 1845
Qy 3788 GATTATGTCGACCAAAAGCGGCATGCTGCT----- 3819
Db 1844 GATTATCAAAAAGGATCTTCACTAGATCTTTTAAATTAAGAAAGATTTTAAATCAA 1785
Qy 3820 -----CCCACTCTCGAGTTCCGGG 3840
Db 1784 TCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1725
Qy 3841 GATGATGATGCGGATGAGCGGCTGCTGTTTCTGATGATGCGAGATTTGATGATGATG 3900
Db 1724 CGAGCCCTGAGCTTCAACCCGAACCTTGGGGGATGAGGATTAAGAAAGAAAGCGG 1665
Qy 3901 -----TAGAATCTCGGAGAGTCTGTCAGCTCAGGACAGCTGAAACCAAC 3946
Db 1664 CGAATGAGCCCAATGAGGATCTCGAGGAGATTCAGAGATGACAGCCTGAGACCGAA 1605
Qy 3947 TCGGAGGAGATCGA----- 3961
Db 1604 CCGCGGTTTATGAACAAACGACCAACCGTGGCTTTATTTCTGCTTTTATTTGCGG 1545
Qy 3962 -----GCCCG 3967

QY 3733 ACGGGCTGACGCTGATGGAAGAAAGAACTCAAGTAAAGGATTTTGTGATGATTA 3792
 DB 4024 ACGGGCTGACGCTGATGGAAGAAAGAACTCAAGTAAAGGATTTTGTGATGATTA 3965
 QY 3793 TCGTCGACCAAGGCGCATGTCCT----- 3819
 DB 3964 TCAAAAAGATCTTCACTAGATCCTTTAAATTAAATGAATTTAAATCATCTAA 3905
 QY 3820 -----CCCCACTCTGACGTTGGGGGCGATG 3845
 DB 3904 AGTATATATAGTAACTGAGGCTATGAGGCGCTGCGCCCGACGTTGGCTGCGAGC 3845
 QY 3846 GATGCGCGGATGACCGCTGCTGCTTCTGATGTCGACGGAATTGACGCGG----- 3900
 DB 3844 CTTGGGCTTCACTCGGAATTTGGGGGGTGGGGGGGGAAGAAAGCGGGCGTAT 3785
 QY 3901 -----TAGAATCCGCGAGGTCGTCAGCCTCAGGAGAGAGTGAACCAATCGCG 3951
 DB 3784 TGGCCCAATGGGGTCTCGGTGGGGTATCGACAGAGTCCAGCGCTGGACCGAACCCG 3725
 QY 3952 AGGGGATCGA----- 3961
 DB 3724 CGTTATGAAACAAACGACCAACGCGGCTTTATCTGCTTTTATATGCGGTATA 3665
 QY 3962 -----GCCCGGGGTGG 3972
 DB 3664 GCGCGGCTTCCCTCCGATTTGTCCTTCCGTGTTTCACTGATGACCTCCCTTAGGGTGG 3605
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 DB 3604 GCGAAGAACTTCAGCATGAGATTCGCCGCTGAGAGATCATCCAGCGGCGTCCCGAAA 3545
 QY 4033 ACGATTCGGAAGCCCACTTTCTATAGAAGCGCGGTGGAATGGAATCTCTGATGCG 4092
 DB 3544 ACGATTCGGAAGCCCACTTTCTATAGAAGCGCGGTGGAATGGAATCTCTGATGCG 3485
 QY 4093 AGGTTGGGCGTGGCTTGGTGGTCAATTCGAACCCGAGTCCGCTCAGAAAGAACTCGT 4152
 DB 3484 AGGTTGGGCGTGGCTTGGTGGTCAATTCGAACCCGAGTCCGCTCAGAAAGAACTCGT 3425
 QY 4153 CAAAGAGCGATAGAAAGCGATGCGCTGCGAATCGGAGCGGCGATACCGTAAAGCA 4212
 DB 3424 CAAAGAGCGATAGAAAGCGATGCGCTGCGAATCGGAGCGGCGATACCGTAAAGCA 3365
 QY 4213 GGAAGCGGTGAGCCCATTCGCGCCCAAGCTTTCAAGCAATTCAGCGGTAGCCCTA 4272
 DB 3364 GGAAGCGGTGAGCCCATTCGCGCCCAAGCTTTCAAGCAATTCAGCGGTAGCCCTA 3305
 QY 4273 TGTCTGATAGCGGTGCGCCACACCCAGCGGCGACAGTGCATGAATTCAGAAAGCGGC 4332
 DB 3304 TGTCTGATAGCGGTGCGCCACACCCAGCGGCGACAGTGCATGAATTCAGAAAGCGGC 3245
 QY 4333 CATTTTCACCATGATATTTGGGCAAGCAAGGATGCGATGGGTCAAGACGATCTTGC 4392
 DB 3244 CATTTTCACCATGATATTTGGGCAAGCAAGGATGCGATGGGTCAAGACGATCTTGC 3185
 QY 4393 CGTGGGCGATGCGGCGCTTGAAGCTTGGGGAACATTTGGGCGGCGAGCCCTGATGCT 4452
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 QY 4453 CTTGCTCAGATCATCTGATGACAAAGACCGGCTTCATCCGATGAGTCTGCTGCA 4512
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 QY 4513 TGGCATGTTTGGTGTGATGCAATGGGAGGTAGCGGATCAAGCGTATGACCGCC 4572
 DB 3064 TGGCATGTTTGGTGTGATGCAATGGGAGGTAGCGGATCAAGCGTATGACCGCC 3005
 QY 4573 GCATTCGATGACGATGATGATCTTTCTGCGAGAGAGCAAGGTGATGATGACGAGAT 4632
 DB 3004 GCATTCGATGACGATGATGATCTTTCTGCGAGAGAGCAAGGTGATGATGACGAGAT 2945
 QY 4633 CTTGCCCGGACCTTGGCCCAATGACAGCGATCCCTTCCGCTTCAGTGACAAAGTCA 4692

DB 2944 CTTGCCCGGACCTTGGCCCAATGACAGCGATCCCTTCCGCTTCAGTGACAAAGTCA 2885
 QY 4693 GCAACGCTGCGAGAGAACCGCCGTGCGGCAAGCAATGACCGCGCTGCTGCT 4752
 DB 2884 GCAACGCTGCGAGAGAACCGCCGTGCGGCAAGCAATGACCGCGCTGCTGCT 2825
 QY 4753 GCAATGCTTCAAGGACCGGACAGGTGCTGTCGAAAGAAACCGGGCGCCCTGCG 4812
 DB 2824 GCAATGCTTCAAGGACCGGACAGGTGCTGTCGAAAGAAACCGGGCGCCCTGCG 2765
 QY 4813 CTGACAGCCGGAACACGCGGCGATGAGACCGGATGCTGTTGTGTCGATGAC 4872
 DB 2764 CTGACAGCCGGAACACGCGGCGATGAGACCGGATGCTGTTGTGTCGATGAC 2705
 QY 4873 CGATATGCTTCTACCCCAAGCGCGGAGAACCTGCGTGAATCATCTTTGATCA 4932
 DB 2704 CGATATGCTTCTACCCCAAGCGCGGAGAACCTGCGTGAATCATCTTTGATCA 2645
 QY 4933 TGGAAAGATCCTCATCTGCTCTTGAATCATCTTG 4971
 DB 2644 TGGAAAGATCCTCATCTGCTCTTGAATCATCTTG 2606

RESULT 14
 US-09-796-575-5/c
 ; Sequence 5, Application US/09796575
 ; Patent No. 663671
 ; GENERAL INFORMATION:
 ; APPLICANT: Genesegues, Inc.
 ; TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD
 ; FILE REFERENCE: G332.12-0001
 ; CURRENT APPLICATION NUMBER: US/09/796,575
 ; PRIORITY FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: US 60/185,282
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 5
 ; LENGTH: 4992
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Supplied by BD Biosciences Clontech of Palo Alto, California
 US-09-796-575-5

Query Match 29.7%; Score 1569.8; DB 3; Length 4992;
 Best local Similarity 86.3%; Pred. No. 0;
 Matches 1847; Conservative 0; Mismatches 112; Indels 180; Gaps 3;
 QY 3013 AAGCGGTATATACGTTATTCACAGATCAGGAGATGACGAGAAAGAAATGATGAGCA 3072
 DB 4988 ATGGCGATATACGTTATTCACAGATCAGGAGATGACGAGAAAGAAATGATGAGCA 4929
 QY 3073 AAAGCGAGAAAGCGCAGAAACCGTAAAGGCGCGTGTGCGGTTTTCATAGG 3132
 DB 4928 AAAGCGAGAAAGCGCAGAAACCGTAAAGGCGCGTGTGCGGTTTTCATAGG 4869
 QY 3133 CTCGCGCCCTTACAGCATCAGAAATTCAGCGTCAAGTAAAGGTGGCGAAACCG 3192
 DB 4868 CTCGCGCCCTTACAGCATCAGAAATTCAGCGTCAAGTAAAGGTGGCGAAACCG 4809
 QY 3193 ACAAGCATTAAGATACAGAGCGTTTCCCGTGAAGCGCTCGTGCCTCTCTGTT 3252
 DB 4808 ACAAGCATTAAGATACAGAGCGTTTCCCGTGAAGCGCTCGTGCCTCTCTGTT 4749
 QY 3253 CCGACCTGCGGCTTACCGGATCCTGTCGCTTCTCCCTTCCGGAAGCGTGGCGCTT 3312
 DB 4748 CCGACCTGCGGCTTACCGGATCCTGTCGCTTCTCCCTTCCGGAAGCGTGGCGCTT 4689
 QY 3313 TCTCATAGCTCAGCGCTGTAGTATCTCAGTTGCGGTGATAGTCTTCCGCTCAAGCTGGCG 3372
 DB 4688 TCTCATAGCTCAGCGCTGTAGTATCTCAGTTGCGGTGATAGTCTTCCGCTCAAGCTGGCG 4629

QY 3373 TGTGTGACGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGTAACTATGCTTT 3432
DB 4628 TGTGTGACGAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGTAACTATGCTTT 4569
QY 3433 GAGTCCAAACCCCGGTAAAGACACGATTTATCGCACTGGCAGACGCACTGGTAAACAGATT 3492
DB 4568 GAGTCCAAACCCCGGTAAAGACACGATTTATCGCACTGGCAGACGCACTGGTAAACAGATT 4509
QY 3493 AGCAGAGGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGTGGCTTAACTACGGC 3552
DB 4508 AGCAGAGGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGTGGCTTAACTACGGC 4449
QY 3553 TACACTAGAAAGAACAGTATTTGGTATCTGCGCTCTGCTAGACAGTTACTTCCGAAAA 3612
DB 4448 TACACTAGAAAGAACAGTATTTGGTATCTGCGCTCTGCTAGACAGTTACTTCCGAAAA 4389
QY 3613 AGAGTTGGTAGCTCTTGTATCCGCAAAACAAACCAACCGCTGTAGCGGTGTTTTTGT 3672
DB 4388 AGAGTTGGTAGCTCTTGTATCCGCAAAACAAACCAACCGCTGTAGCGGTGTTTTTGT 4329
QY 3673 TGCAGACGACGATTAACCGCGGAAAAAGATCTCAAGAGATCTTTGATCTTTTCT 3732
DB 4328 TGCAGACGACGATTAACCGCGGAAAAAGATCTCAAGAGATCTTTGATCTTTTCT 4269
QY 3733 ACGGGGCTGACGCTCACTGAGAACGAAAACTCACGTTAAGGGATTTGGTCAAGAGTTA 3792
DB 4268 ACGGGGCTGACGCTCACTGAGAACGAAAACTCACGTTAAGGGATTTGGTCAAGAGTTA 4209
QY 3793 TGTGTGACCAAGCGGCGCATCTGCTT----- 3819
DB 4208 TCAAAAAGGATCTTCACTAGATCTTTTAAATTAAGATTTTAAATCAATCTAA 4149
QY 3820 -----CCCACTCTGCACTTGGGGGCACTG 3845
DB 4148 AGTATATATAGTAACTGAGGCTATGCGAGGCTGCGCCGCCACGCTGCTCGAGC 4089
QY 3846 GATGCGCGGATAGCCGCTGCTGTTTCCGTAAGCGATTCGATTTGCACTGCGG----- 3900
DB 4088 CCTGGGCTTCAACCCGAACCTTGGGGGGTGGGGTGGGAAAAAGAAAGAAACGGGGCGTAT 4029
QY 3901 -----TAGAACCTCCGAGAGTCTGTCAGCCTCAGGACGACGACGACCACTACGCG 3951
DB 4028 TGGCCCAATGAGGCTGCTGGGTATGACAGAGTCCAGCCTGGGACCGAACCCG 3969
QY 3952 AGGGGATGA----- 3961
DB 3968 CGTTTATGAACAAACGACCAACCGTGCCTTTATCTGTCTTTTATGCGCTCATTA 3909
QY 3962 -----GCCCGGGGTG 3972
DB 3908 GCGCGGGTCTCTCCGATTTGTCTCTTCCGTGTTTCACTTACGCTTCCCTCCCTAGAGGTGG 3849
QY 3973 GCGAAGAACTCAGCATGAGATCCCGCGCTGAGAGATCATCAGCCGCGCTCCGGA 4032
DB 3848 GCGAAGAACTCAGCATGAGATCCCGCGCTGAGAGATCATCAGCCGCGCTCCGGA 3789
QY 4033 ACGATTCCGAAGCCCACTTTCAATGAAGCGGCGGTGGAATCGAAATCTCTGTATGGC 4092
DB 3788 ACGATTCCGAAGCCCACTTTCAATGAAGCGGCGGTGGAATCGAAATCTCTGTATGGC 3729
QY 4093 AGGTTGGGCGTCTGCTGCTGCTATTTGAAACCCCAAGTCCCGCTAGAAAGAACTGT 4152
DB 3728 AGGTTGGGCGTCTGCTGCTGCTATTTGAAACCCCAAGTCCCGCTAGAAAGAACTGT 3669
QY 4153 CAAGAAGCGATAGAAAGCGATGCGCTCGATCGGAGCGCGCATACCGTAAAGCAAGA 4212
DB 3668 CAAGAAGCGATAGAAAGCGATGCGCTCGATCGGAGCGCGCATACCGTAAAGCAAGA 3609
QY 4213 GGAAGCGGTCAAGCCATTCGCGCCCACTCTTCAAGCAATATCACGGGTAGCCCAAGCTTA 4272
DB 3608 GGAAGCGGTCAAGCCATTCGCGCCCAAGCTCTTCAAGCAATATCACGGGTAGCCCAAGCTTA 3549

QY 4273 TGTCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGATCCAGAAAAAGCGC 4332
DB 3548 TGTCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGATCCAGAAAAAGCGC 3489
QY 4333 CATTTTCAACATGATATTTGGCAAGGACATGCGCATGGGTCAAGAGATCTTCG 4392
DB 3488 CATTTTCAACATGATATTTGGCAAGGACATGCGCATGGGTCAAGAGATCTTCG 3429
QY 4393 CGTGGGATAGCGGCTTTGAGCCCTGGGAAACAGTTCGGCTGGCCGAGCCCTGATGT 4452
DB 3428 CGTGGGATAGCGGCTTTGAGCCCTGGGAAACAGTTCGGCTGGCCGAGCCCTGATGT 3369
QY 4453 CTTCGTCCAGATCATCTGATGACAAAGCGGCTTCATCCAGTACGATGCTGCTCGA 4512
DB 3368 CTTCGTCCAGATCATCTGATGACAAAGCGGCTTCATCCAGTACGATGCTGCTCGA 3309
QY 4513 TGCATGTTTGGCTTGTGTCGAAATGGGACAGTACCGGATCAAGCGTATGACCGCC 4572
DB 3308 TGCATGTTTGGCTTGTGTCGAAATGGGACAGTACCGGATCAAGCGTATGACCGCC 3249
QY 4573 GCATTGCAATCAAGCATATGATATCTTCTGGCAGAGCAAGGTGATGACAGAGAT 4632
DB 3248 GCATTGCAATCAAGCATATGATATCTTCTGGCAGAGCAAGGTGATGACAGAGAT 3189
QY 4633 CTGCCCCGACCTTCCGCAATAGCAGCAGTCCCTCCGCTCAGTGAACAAGTGA 4692
DB 3188 CTGCCCCGACCTTCCGCAATAGCAGCAGTCCCTCCGCTCAGTGAACAAGTGA 3129
QY 4693 GCACAGCTGCGCAAGAAACGCGCTGTCGAGCAGCAGATAGCCGCTGCTGCTCT 4752
DB 3128 GCACAGCTGCGCAAGAAACGCGCTGTCGAGCAGCAGATAGCCGCTGCTGCTCT 3069
QY 4753 GCATTCAATTAAGGACACCGGACAGTGTGTTTGAACAAAAAGAACCGGGCGCTTCG 4812
DB 3068 GCATTCAATTAAGGACACCGGACAGTGTGTTTGAACAAAAAGAACCGGGCGCTTCG 3009
QY 4813 CTGACGCGGAAACACCGCGGATCAGAGCAGCGATTGTCTGTTGCGCAGTATAGC 4872
DB 3008 CTGACGCGGAAACACCGCGGATCAGAGCAGCGATTGTCTGTTGCGCAGTATAGC 2949
QY 4873 CGAATAGCTTCCACCCCAACCGGCGGAGAACTGCTGCAATCATCTTGTTCATCA 4932
DB 2948 CGAATAGCTTCCACCCCAACCGGCGGAGAACTGCTGCAATCATCTTGTTCATCA 2889
QY 4933 TGCAGAACGATCTCATCTCTTCTTGTGATCAATCTTG 4971
DB 2888 TGCAGAACGATCTCATCTCTCTTGTGATCAATCTTG 2850

RESULT 15
US-09-393-483A-1/C
; Sequence 1, Application US/09393483A
; Patent No. 6689936
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Amano, Satoshi
; APPLICANT: Kishimoto, Uiro
; APPLICANT: Nishiyama, Toshio
; APPLICANT: Ehama, Ritsuko
; TITLE OF INVENTION: METHODS FOR EVALUATING A COMPOUND FOR
; TITLE OF INVENTION: ITS EFFECT ON SKIN
; FILE REFERENCE: 10287-054001
; CURRENT APPLICATION NUMBER: US/09/393,483A
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 09/070,436
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/069,945
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5069
; TYPE: DNA

ORGANISM: Homo sapiens
US-09-393-483A-1

Query Match 29.7%; Score 1569.8; DB 3; Length 5069;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1847; Conservative 0; Mismatches 112; Indels 180; Gaps 3;

QY 3013 AAGCGGTATATACGGTTATTCACAGAAATCAGGGATATACGAGAAAGAAACATGTGACCA 3072
DB 5065 ATGGCGGTATATACGGTTATTCACAGAAATCAGGGATATACGAGAAAGAAACATGTGACCA 5006
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DB 5005 AAAAGCCAGCAAAAGCCAGGAAACCGTAAAAAAGCCGGTTCGCGGTTTTTTCATAGG 4946
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DB 4525 TACACTAGAAGAAAGATTTTGTATCTGCGCTGCTGAGCGCAGTTACTTGGGAAA 4466
QY 3613 AGAGTTGGTACCTCTGATTCGCGCAAAACAACCGCTGTAGCGGTGTTTTTTTGT 3672
DB 4465 AGAGTTGGTACCTCTGATTCGCGCAAAACAACCGCTGTAGCGGTGTTTTTTTGT 4406
QY 3673 TGCAGAGCGAGATTAACCGCGCAAAAAAAGAGTCTCAAGAGATCTTATATCTTTTCT 3732
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QY 3733 ACGGGGTCTGACGCTCAGTGAACGAAAACTCAGTTAAGGATTTTGTATGAGATTA 3792
DB 4345 ACGGGGTCTGACGCTCAGTGAACGAAAACTCAGTTAAGGATTTTGTATGAGATTA 4286
QY 3793 TCGTCGACCAAAAGCGGCATGTGCTT----- 3819
DB 4285 TCAAAAAGATCTTACCTAGATCTTTTAAATTAATAAGTAAATCAATCAAA 4226
QY 3820 -----CCGACCTCTGCAATGTGGGGGCAATG 3845
DB 4225 AGTATATATGATTAAGTGAAGCTATGAGCGGCTTCCGCGCGCACTGTGCGAGC 4166
QY 3846 GATGCGCGGATTAAGCGCTGTGTTTCTGTGATGCGCAGATTTTGAATGCGG----- 3900
DB 4165 CTTGGGCTTCAACCGCACTTGGGGGGTGGGGTGGGAAAAAGAAAGAAACGCGGCGTAT 4166
QY 3901 -----TGAACCTCGCGAGGTGTCGACGCTCAGGCAAGCACTGAACCAACTCGCG 3951

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QY 3952 AGGGATCA----- 3961
DB 4045 CGTTTATGAACAACGACCCCAACACCGTGCCTTTTATTTGTTATGCGCTCATTA 3986
QY 3962 -----GCCCGGGGTG 3972
DB 3985 GCGCGGGTCTTCCGGTATTTGCTCTTCCTTCGTTTCAAGTACCTCCCTCAGAGGTGG 3926
QY 3973 GCGAAGAACTCCAGATGATATCCCGCGCTGAGGATCATCCAGCGCGTCCGAAA 4032
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DB 3325 GCAATTCATGAGCAATGATGATCTTCTCGGCAAGAGCAAGTGAAGAGAT 3266
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DB 3025 CGAATAGCTCTTCAACCAAGCGGCGGAGAACTGCGTGCATTCATCTTGTTCATCA 2966

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Oy		4933	TGGCAACGATCTCATCCTGTCTTGCATTAGACTTTG	4971
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Job time : 654 secs

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Qy 421 GTATTTAAGTCCAGCTCGATCAATATAAGCCATTGTGACATTCGCAATTGGTGTG 480
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Qy 541 CTGCTGCCGCTGGCTGCTTCCGGGTCTTCGGAAGGCCCGCGCGCGCGCGCTTC 600
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Db	2521	CTTACCAACTGAGAACTACTGCAACTAGGCCCAACAATAACCTGTCCACCCTCTGCA	2580
QY	2581	ATGAATTAACCTTTGAAGAGCACTACAAGTTGTGTATACATGTGTCAATGTGCATATG	2640
Db	2581	ATGAATTAACCTTTGAAGAGCACTACAAGTTGTGTATACATGTGTCAATGTGTCAATGTG	2640
QY	2641	TGTCGCGGGGGAGCATATAGTGGGCTGACTGAGTGTGCGCGCTTAATCTATCTGGCA	2700
Db	2641	TGTCGCGGGGGAGCATATAGTGGGCTGCTGAGATGTGCGCGCTTAATCTATCTGGCA	2700
QY	2701	GCTGTCTAGACGTATCATGTGATAGCTGTTCCTGTGTGAATTTGTAATCCGCTACA	2760
Db	2701	GCTGTCTAGACGTATCATGTGATAGCTGTTCCTGTGTGAATTTGTAATCCGCTACA	2760
QY	2761	ATTCCACAACAATCGAGCCGGGAAGCAATAAGTATAAGCTGGGGGCTTAATGTAGTG	2820
Db	2761	ATTCCACAACAATCGAGCCGGGAAGCAATAAGTATAAGCTGGGGGCTTAATGTAGTG	2820
QY	2821	AGCTAACTCACTTAATTATGCGTTGGGCTCACTGCGCCGCTTTCAGTCGGAGAACTGTG	2880
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QY	2881	TGCCAGCTGCATTATTAATGAATGGCCCAACGCGCGGAGAGGCGGTTTGCGTAATGGCGC	2940
Db	2881	TGCCAGCTGCATTATTAATGAATGGCCCAACGCGCGGAGAGGCGGTTTGCGTAATGGCGC	2940
QY	2941	TCTTCGCGTTTCTGTGCTCACTGACTGTGGCTGTGCTGTTCGGCTGTGCGGTGCGGAGCGGTA	3000
Db	2941	TCTTCGCGTTTCTGTGCTCACTGACTGTGGCTGTGCTGTTCGGCTGTGCGGTGCGGAGCGGTA	3000
QY	3001	TCAGCTCACTAAAGGCGGTATAACGTTATCCACAGAAATCAGGGGATATACGACGAGAAAG	3060
Db	3001	TCAGCTCACTAAAGGCGGTATAACGTTATCCACAGAAATCAGGGGATATACGACGAGAAAG	3060
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Db	3061	AACATGTAGCAAAAAGGCCACAAAAGGCCAGAAACCGTAAAAAGGCCGCGTTGCTGGCG	3120
QY	3121	TTTTTCCATAGGCTCCGCCCCCTGACGAGCATACAAAAATGACGCTCAAGTCAGAGG	3180
Db	3121	TTTTTCCATAGGCTCCGCCCCCTGACGAGCATACAAAAATGACGCTCAAGTCAGAGG	3180
QY	3181	TGGCGAAACCCGACGAGACTATAAAGATACACAGGCGTTCCCGTGAAGGTCCTGTG	3240
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QY	3241	CGCTCTCCTGTTCCGACCCCTGACCGGATACCGGATACGTCGCGCTTTCCTCCCTCGGGA	3300
Db	3241	CGCTCTCCTGTTCCGACCCCTGACCGGATACCGGATACGTCGCGCTTTCCTCCCTCGGGA	3300
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Db	3301	AGCGTGGGCTTCTCATAGCTCAACGCTGTAGGTATCTCAAGTTGGGTAGGTGCTTGC	3360
QY	3361	TCCAAGCTGGGCTGTGTCAGAAACCCCGGTTAGGCCGACCGCTGCGGCTTAATCCGGT	3420
Db	3361	TCCAAGCTGGGCTGTGTCAGAAACCCCGGTTAGGCCGACCGCTGCGGCTTAATCCGGT	3420
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Db	3421	AACATAGCTCTTGAAGTCCAAACCGGTAAAGACACACTTAATGCGCACTGGCAGACGCACT	3480
QY	3481	GGTAAACAGGATTTAGCAGAGCGAGGTATGTAGGCGGTGTACAGATTTCTTGAAGTGGTGG	3540
Db	3481	GGTAAACAGGATTTAGCAGAGCGAGGTATGTAGGCGGTGTACAGATTTCTTGAAGTGGTGG	3540
QY	3541	CCTAACTACGCTCACTAGAAAGAAAGTATTTGGTATTCGCGCTGTGAGAGCCAGTT	3600
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Qy	3661	GGTTTTTTTGTGTAAGCAGATTAACGGGCAAGAAAAAGATCTCAAGAAATCCT	3722
Db	3661	GGTTTTTTTGTGTAAGCAGATTAACGGGCAAGAAAAAGATCTCAAGAAATCCT	3722
Qy	3721	TTGATCTTTTCTACCGGGGTCTGACGCTCAGTGGAAACGAAAACTCAGTTAAGGATTTTG	3780
Db	3721	TTGATCTTTTCTACCGGGGTCTGACGCTCAGTGGAAACGAAAACTCAGTTAAGGATTTTG	3780
Qy	3781	GTCAATGAGATTATCGTCCACCAAGCGGCCATCGTGCTCCCACTCTCGAAGTTGAGG	3840
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Db	3841	GCATGGAATGCGCGGATACCGCGCTGTGGTTTCTGGAATGCCGACGGAATTTGACATGCCGG	3900
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Qy	4201	CGTAAAGACAGAGAAAGGGGTCAAGCCATTTGCGCGCCAAAGCTTTTCAGCAATATCACGGG	4260
Db	4201	CGTAAAGACAGAGAAAGGGGTCAAGCCATTTGCGCGCCAAAGCTTTTCAGCAATATCACGGG	4260
Qy	4261	TAGCCAAACGCTATGTCCTGATAGAGGGTCCGCGACACCCAGCGGCGCACAGTCGATGTAATC	4320
Db	4261	TAGCCAAACGCTATGTCCTGATAGAGGGTCCGCGACACCCAGCGGCGCACAGTCGATGTAATC	4320
Qy	4321	CAGAAAAGCGGCAATTTTTCACACATGATATTGCGCAAGCAGGCAATCGCATGAGGTCAAGA	4380
Db	4321	CAGAAAAGCGGCAATTTTTCACACATGATATTGCGCAAGCAGGCAATCGCATGAGGTCAAGA	4380
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Db	4381	CGAAGTCTCGCCGCTCGGCGCATGCGCGCTTGGAACCTGCGCCAAACAGTTCCGCTGGCGGA	4440
Qy	4441	GCCCTCGATGCTCTTGGTCCGACATCAATTCGATGCAAGACCGGGCTTCCATCCGAGTAC	4500
Db	4441	GCCCTCGATGCTCTTGGTCCGACATCAATTCGATGCAAGACCGGGCTTCCATCCGAGTAC	4500
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Db	4501	GTGCTCGCTCAGTCGATGTTTCGCTTGATGGTGAATGCGCAGTATAGCCGATCAACGCG	4560
Qy	4561	TATGACGCGCGCGCATTTGCATCAACCATGATGATATTCTTCGCGCAGGACAAAGTGAG	4620
Db	4561	TATGACGCGCGCGCATTTGCATCAACCATGATGATATTCTTCGCGCAGGACAAAGTGAG	4620
Qy	4621	ATGACAGGAGATTCGTGCGCGGCGACTTGCCCAATACACGACAGTCCCTTCGCGCTTAG	4680
Db	4621	ATGACAGGAGATTCGTGCGCGGCGACTTGCCCAATACACGACAGTCCCTTCGCGCTTAG	4680
Qy	4681	TGAACAGTCAGACAGCTGCGCAAGAAACGCGCTGTTGGCCAGCAGATAGCCGCG	4740
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DB 6991 GAGATTATCAAAAAGGATCTTCACTGATCTT----- 7024
QY 3846 GATGGCCGGAATAGCCGCTGCTGTTTCTGATGCGGACGGAATTGCACTCCGGTAGAA 3905
DB 7025 ----- 7024
QY 3906 CTCCGCGAGGTCGTCAAGCCTCAGGCAAGCTGAAACCACTCGGAGGGGATCGAGCCC 3965
DB 7025 -----TT 7026
QY 3966 GGGGTGGGGAAGAACTCCAGCATGATCCCGGCTGAGAGATCATCAAGCCGGCTC 4025
DB 7027 GGGGTGGGGAAGAACTCCAGCATGATCCCGGCTGAGAGATCATCAAGCCGGCTC 7086
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QY 4746 TCGTCTGCAAGTTCAATGAGGCAACCGGACAGGTGCTTTCGACAAAAAGAACCGGGGCG 4805
DB 7807 TCGTCTGCAAGTTCAATGAGGCAACCGGACAGGTGCTTTCGACAAAAAGAACCGGGGCG 7866
QY 4806 CCGTGGCGTGAACAGCGCGGAAACAGCGCGGCAATCAAGAGCGCGATGCTGTTGCGCCAG 4865
DB 7867 CCGTGGCGTGAACAGCGCGGAAACAGCGCGGCAATCAAGAGCGCGATGCTGTTGCGCCAG 7926
QY 4866 TCATAGCCGAATAGCTCTTCCACCCAAAGCGGCGGAGAACTCGGTGATCATCTTGT 4925

DB 7927 TCATAGCCGAATAGCTCTTCCACCCAAAGCGCGGAAACCTGCGTCAATCATCTTGT 7986
QY 4926 TCATATGCGGAACAGATCTCATATCTGTTCTTGTATGATGATCTTATCCCTGGCCAT 4985
DB 7987 TCATATGCGGAACAGATCTCATATCTGTTCTTGTATGATGATCTTATCCCTGGCCAT 8046
QY 4986 CAGATCTTGGCGGGAAGAAAGCCATTCAGATTACTTTGCAAGGCTTCCCACTTACCA 5045
DB 8047 CAGATCTTGGCGGGAAGAAAGCCATTCAGATTACTTTGCAAGGCTTCCCACTTACCA 8106
QY 5046 GAGGCGGCCCAAGCTGCAATTCGCTTCCGTTGCTGTCATPAAACGCCAGCTAGC 5105
DB 8107 GAGGCGGCCCAAGCTGCAATTCGCTTCCGTTGCTGTCATPAAACGCCAGCTAGC 8166
QY 5106 TATGCGCATGTAAGCCCACTGCAAGCTACTGCTTCTTCTTGGCGTTCCTTCCCTT 5165
DB 8167 TATGCGCATGTAAGCCCACTGCAAGCTACTGCTTCTTCTTGGCGTTCCTTCCCTT 8226
QY 5166 GTCCAGATAGCCCAAGTACTGATCAATTCGCGGTGACAGCCGTTCTGGGACTGGCT 5225
DB 8227 GTCCAGATAGCCCAAGTACTGATCAATTCGCGGTGACAGCCGTTCTGGGACTGGCT 8286
QY 5226 TTCTACGTGTTCCGCTTCTTCTTACGAGCCCTTGGCGCCCTGAGTGTGCTGGGAGCGTG 5283
DB 8287 TTCTACGTGTTCCGCTTCTTCTTACGAGCCCTTGGCGCCCTGAGTGTGCTGGGAGCGTG 8344

RESULT 3
US-10-841-796-33
; Sequence 33, Application US/10841796
; Publication No US20040237138A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Biotechnology Corporation
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Nordine, Chiekh
; APPLICANT: Fisher, Dane
; APPLICANT: Thompson, Rebecca
; TITLE OF INVENTION: A method of increasing yield in a plant
; FILE REFERENCE: Docket number 38-21 (15691)B
; CURRENT FILING DATE: 2004-07-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 11546
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid containing construct for corn transformation
US-10-841-796-33

Query Match 42.4%; Score 2240; DB 8; Length 11546;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 2409; Conservative 0; Mismatches 25; Indels 144; Gaps 1;

QY 2706 CTAGAGTATCATGATGATGCTGTTCTCTGTGAAATTTGATTCGCTCACAATTC 2765
DB 9108 CTGGCGTAATCATGATGATGCTGTTCTCTGTGAAATTTGATTCGCTCACAATTC 9167
QY 2766 ACACAATCATGAGCGGGAAGCAATTAAGTGAAGCCTGGGGTGCCTAAAGAGACTA 2825
DB 9168 ACACAATCATGAGCGGGAAGCAATTAAGTGAAGCCTGGGGTGCCTAAAGAGACTA 9227
QY 2826 ACTCACATTAATGCTGTTGGCTCACTGCCGCTTTCAGTCCGGAACCTGTGTCGA 2885
DB 9228 ACTCACATTAATGCTGTTGGCTCACTGCCGCTTTCAGTCCGGAACCTGTGTCGA 9287
QY 2886 GCTGCATTAATGAATCGGCCAAGCGCGGGAAGAGCGGTTTGCGTATTTGGCGCTCTTC 2945
DB 9288 GCTGCATTAATGAATCGGCCAAGCGCGGGAAGAGCGGTTTGCGTATTTGGCGCTCTTC 9347
QY 2946 CGCTTCTGCTCACTGACTCGCTGCGCTGCTGCTTCCGCTGCGGAGCGGATACAGC 3005

Db 9348 CGCTTCTCGCTAATGACTCGTGGCTGGCTGTTCCGGCTGGCGGAGCGGATACAG 9407
Qy 3006 TCACTCAAAAGCGGTAAATACGTTATTCACAGATCAAGGAGTAAAGCGAAAGAACT 3065
Db 9408 TCACTCAAAAGCGGTAAATACGTTATTCACAGATCAAGGAGTAAAGCGAAAGAACT 9467
Qy 3066 GTAGGCAAAAGCGGAGCAAAAGCGGAAACCGTAAAAAGCGCGCTTGGCGTTT 3125
Db 9468 GTAGGCAAAAGCGGAGCAAAAGCGGAAACCGTAAAAAGCGCGCTTGGCGTTT 9527
Qy 3126 CCATAGGCTCGCGCCCTTGAAGATCAAGAGATCAAAATTCAGCTCAAGTCAAGGTGGG 3185
Db 9528 CCATAGGCTCGCGCCCTTGAAGATCAAGAGATCAAAATTCAGCTCAAGTCAAGGTGGG 9587
Qy 3186 AAACCCGACAGACTAATAAGATTCAGGAGGTTCCCGTGAAGCTCCCTGGCGCTC 3245
Db 9588 AAACCCGACAGACTAATAAGATTCAGGAGGTTCCCGTGAAGCTCCCTGGCGCTC 9647
Qy 3246 TCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTGGGAAAGCT 3305
Db 9648 TCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTGGGAAAGCT 9707
Qy 3306 GGGCGTTTCTATAGTCAAGCTGATGATCTCAAGTTCGATGAGTGGTGGCTCA 3365
Db 9708 GGGCGTTTCTATAGTCAAGCTGATGATCTCAAGTTCGATGAGTGGTGGCTCA 9767
Qy 3366 GCTGGGCTGTGACGCAACCCCGTTACGCGGACGCGCTGCGCTTATCCGTAATA 3425
Db 9768 GCTGGGCTGTGACGCAACCCCGTTACGCGGACGCGCTGCGCTTATCCGTAATA 9827
Qy 3426 TCGTTGATGATCAACCCGTTAAGACAGACTTATCCGCTGCGACAGCACTGGTAA 3485
Db 9828 TCGTTGATGATCAACCCGTTAAGACAGACTTATCCGCTGCGACAGCACTGGTAA 9887
Qy 3486 CAGATTGACAGAGGAGATGATGAGGCGTCAAGAGTTCTTGAAGTGGTGGCTAA 3545
Db 9888 CAGATTGACAGAGGAGATGATGAGGCGTCAAGAGTTCTTGAAGTGGTGGCTAA 9947
Qy 3546 CTACGGCTACATAGAAAGAGATTTGATCTGCGCTCTGCTGAAGCCAGTTACCT 3605
Db 9948 CTACGGCTACATAGAAAGAGATTTGATCTGCGCTCTGCTGAAGCCAGTTACCT 10007
Qy 3606 CGGAAAGAGTTGATGATCTGATCCGGGAAACAAACCCGCTGATAGCGGAGTT 3665
Db 10008 CGGAAAGAGTTGATGATCTGATCCGGGAAACAAACCCGCTGATAGCGGAGTT 10067
Qy 3666 TTTTGTTCAGACAGAGATTAACGCGAGAAAGAAAGATCTCAAGAGATCTTTGAT 3725
Db 10068 TTTTGTTCAGACAGAGATTAACGCGAGAAAGAAAGATCTCAAGAGATCTTTGAT 10127
Qy 3726 CTTTTCATACGAGGATGATGATCTGATCCGGGAAACAAACCTTGAAGGATTTGGTAT 3785
Db 10128 CTTTTCATACGAGGATGATGATCTGATCCGGGAAACAAACCTTGAAGGATTTGGTAT 10187
Qy 3786 GAGATTATGATGATCCAAAGCGGCAATGCTGCCCTCCCACTCTCAAGTTCCGGGAGATG 3845
Db 10188 GAGATTATGATGATCCAAAGCGGCAATGCTGCCCTCCCACTCTCAAGTTCCGGGAGATG 10221
Qy 3846 GATGCGGATGATGCGCTGCTGATTCCTGATGCCAGAGATTTGACCTCCGATGA 3905
Db 10222 ----- 10221
Qy 3906 CTCGCGAGGTGCTCAAGCTTACGAGAGCTGAACCAACTCCGAGGGAGTCGAGCCC 3965
Db 10222 -----TT 10223
Qy 3966 GGGGTGGCGAGAACTCCAGATGAGATCCCGCGCTGAGAGATCATCCAGCGGCTC 4025
Db 10224 GGGGTGGCGAGAACTCCAGATGAGATCCCGCGCTGAGAGATCATCCAGCGGCTC 10283
Qy 4026 CCGGAAAGCATTCGAGGCTCAAGCTTTATGAAAGCGGCGGTGGATCCAAATCTCG 4085

Db 10284 CCGGAAAGCATTCGAGGCTCAAGCCCAACTTTATAGAAAGCGGCGGTGGATCGAAATCTCG 10343
Qy 4086 TGATGAGAGTTGGGCGTCCGTTGCTGATCTTTCGAAACCCGAGATCCCGCTCGAAG 4145
Db 10344 TGATGAGAGTTGGGCGTCCGTTGCTGATCTTTCGAAACCCGAGATCCCGCTCGAAG 10403
Qy 4146 AACTGTCAAAAGCGATAGAAAGCGATGCGCTGCAATTCGGAGCGGATACCGTAA 4205
Db 10404 AACTGTCAAAAGCGATAGAAAGCGATGCGCTGCAATTCGGAGCGGATACCGTAA 10463
Qy 4206 AGCAGAGAAAGCGATGAGCCATTCGCGCAAGCTCTTTCAGCAATATACGGGTGCC 4265
Db 10464 AGCAGAGAAAGCGATGAGCCATTCGCGCAAGCTCTTTCAGCAATATACGGGTGCC 10523
Qy 4266 AAGCTATGCTCTGATGAGCGTCCGCAACCCGCGGCGCAAGTGGATATCCAGAA 4325
Db 10524 AAGCTATGCTCTGATGAGCGTCCGCAACCCGCGGCGCAAGTGGATATCCAGAA 10583
Qy 4326 AAGCGGCAATTTCCACCATGATATTCGCAAGAGGATCCGATGGGTCAAGAGAA 4385
Db 10584 AAGCGGCAATTTCCACCATGATATTCGCAAGAGGATCCGATGGGTCAAGAGAA 10643
Qy 4386 TCTTGGCGGTGGGATGCGGCGCTTGAAGCTTGGCGAAAGTTGGGCTGGGCGAGCCC 4445
Db 10644 TCTTGGCGGTGGGATGCGGCGCTTGAAGCTTGGCGAAAGTTGGGCTGGGCGAGCCC 10703
Qy 4446 TGAATGCTCTGATCCAGATCAATCTGATCGAACAGACCGGCTTCATCCGATAGTCT 4505
Db 10704 TGAATGCTCTGATCCAGATCAATCTGATCGAACAGACCGGCTTCATCCGATAGTCT 10763
Qy 4506 CGCTGATGCGATGTTTGGCTTGTGTGATGAAATGGGCAAGTACCGGATCAAGCTATG 4565
Db 10764 CGCTGATGCGATGTTTGGCTTGTGTGATGAAATGGGCAAGTACCGGATCAAGCTATG 10823
Qy 4566 AAGCGCGGATGATCAAGGATGATGATGATCTTCTGCGAGAGCAAGGTGAGTAC 4625
Db 10824 AAGCGCGGATGATCAAGGATGATGATGATCTTCTGCGAGAGCAAGGTGAGTAC 10883
Qy 4626 AGGAGATCTGCGCCCGGCACTTCGCCAATAGACAGCTGCTTCCGCTTCACTGACA 4685
Db 10884 AGGAGATCTGCGCCCGGCACTTCGCCAATAGACAGCTGCTTCCGCTTCACTGACA 10943
Qy 4686 AAGTGCAGACAGCTGCGCAAGAAAGCCCGTGTGGCGAGCAGATAGCGGCTGCC 4745
Db 10944 AAGTGCAGACAGCTGCGCAAGAAAGCCCGTGTGGCGAGCAGATAGCGGCTGCC 11003
Qy 4746 TCGTCCGAGTTCATTCAGGGGACCGGACAGGTGCTTGAACAAAGAAACCGGCGC 4805
Db 11004 TCGTCCGAGTTCATTCAGGGGACCGGACAGGTGCTTGAACAAAGAAACCGGCGC 11063
Qy 4806 CCCTGCGCTGACAGCGGAAACAGGCGGATCAGAGCAGCCGATGCTGTTGGCCAG 4865
Db 11064 CCCTGCGCTGACAGCGGAAACAGGCGGATCAGAGCAGCCGATGCTGTTGGCCAG 11123
Qy 4866 TCAATGCGCAATAGCCCTTCACCAAGCGGCGGAGAACTGCGCAATCATCTTGT 4925
Db 11124 TCAATGCGCAATAGCCCTTCACCAAGCGGCGGAGAACTGCGCAATCATCTTGT 11183
Qy 4926 TCAATGCGCAATAGCCCTTCATCTGCTCTTGAATCAGATTTGATCCCTGGCCAT 4985
Db 11184 TCAATGCGCAATAGCCCTTCATCTGCTCTTGAATCAGATTTGATCCCTGGCCAT 11243
Qy 4986 CAGATCTTGGCGGAGAAAGCAATCCAGTTACTTTGAGAGGCTTCCCACTTACCA 5045
Db 11244 CAGATCTTGGCGGAGAAAGCAATCCAGTTACTTTGAGAGGCTTCCCACTTACCA 11303
Qy 5046 GAGGCGCGCCAGCTGCAATTCGAGTTCCGTTGCTGCTCAATAAACCGGCAAGTACG 5105
Db 11304 GAGGCGCGCCAGCTGCAATTCGAGTTCCGTTGCTGCTCAATAAACCGGCAAGTACG 11363
Qy 5106 TATGCGATGTAAGCCCACTGCAAGTAACTGCTTCTCTTGGCGCTTGGCTTCCCT 5165
Db 11364 TATGCGATGTAAGCCCACTGCAAGTAACTGCTTCTCTTGGCGCTTGGCTTCCCT 11423

Query 5166 GTCCAGATAGCCAGTAGTGAATTCATCCGGGGTCAAGACCGTTTCTGCGAGTGGCT 5225
Db 11424 GTCCAGATAGCCAGTAGTGAATTCATCCGGGGTCAAGACCGTTTCTGCGAGTGGCT 11483
Qy 5226 TTCTACGTTCCGCTTCTCTTTAGACGCCCTTCCGCTGAGTGGCTGGCGAGCGTG 5283
Db 11484 TTCTACGTTCCGCTTCTCTTTAGACGCCCTTCCGCTGAGTGGCTGGCGAGCGTG 11541

RESULT 4
US-10-322-360-1/c
; Sequence 1, Application US/10322360
; Publication No. US20030165946A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: A Method for the Complete Chemical
; TITLE OF INVENTION: Synthesis and Assembly of Genes and Genomes
; FILE REFERENCE: P-EA 5511
; CURRENT APPLICATION NUMBER: US/10/322,360
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 09/554,929
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4800
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic plasmid
US-10-322-360-1

Query Match 33.9%; Score 1793.4; DB 6; Length 4800;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1;

Qy 3127 CATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCAGCGCTCAAGTCAAGGTGGCGA 3186
Db 4800 CATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCAGCGCTCAAGTCAAGGTGGCGA 4741
Qy 3187 AACCCGACAGGACTAATAAGATACAGGCGTTTCCCTGGAAGTCCCTGTGGCTCT 3246
Db 4740 AACCCGACAGGACTAATAAGATACAGGCGTTTCCCTGGAAGTCCCTGTGGCTCT 4681
Qy 3247 CCGTTCGACCCCGCTTACCGGATACCTGTCCGCTTTCCTTCCGGAAGCGTG 3306
Db 4680 CCGTTCGACCCCGCTTACCGGATACCTGTCCGCTTTCCTTCCGGAAGCGTG 4621
Qy 3307 GCGCTTCTCATAGCTCAAGCTGATCTCAAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 3366
Db 4620 GCGCTTCTCATAGCTCAAGCTGATCTCAAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 4561
Qy 3367 CTGGGCTGTGTGCAAGACCCCGCTTACCGGATACCTGTCCGCTTTCCTTCCGGAAGCGTG 3426
Db 4560 CTGGGCTGTGTGCAAGACCCCGCTTACCGGATACCTGTCCGCTTTCCTTCCGGAAGCGTG 4501
Qy 3427 CCGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 3486
Db 4500 CCGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 4441
Qy 3487 AGATTTAGCAGAGGAGTATGTAGGCGGTCTACAGGTTCTTGAAGTGGTGGCTTAAC 3546
Db 4440 AGATTTAGCAGAGGAGTATGTAGGCGGTCTACAGGTTCTTGAAGTGGTGGCTTAAC 4381
Qy 3547 TAGGCTTACACTAGAGAAAGATTTGGTATCTGCGCTCTGTAAGCCAGTTACCTTC 3606
Db 4380 TAGGCTTACACTAGAGAAAGATTTGGTATCTGCGCTCTGTAAGCCAGTTACCTTC 4321
Qy 3607 GGAAGAAAGATTTGGTATCTGATCCGGCAAAACCAACCCGCTGGTGAAGCGGTCTTT 3666
Db 4320 GGAAGAAAGATTTGGTATCTGATCCGGCAAAACCAACCCGCTGGTGAAGCGGTCTTT 4261

Qy 3667 TTTGTTTCAAGCAGACAGATTTACGGCGAGAAAAAAGATCTCAGAAGATCTTTGATC 3726
Db 4260 TTTGTTTCAAGCAGACAGATTTACGGCGAGAAAAAAGATCTCAGAAGATCTTTGATC 4201
Qy 3727 TTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCAGCTTAAAGGATTTGGTCAATG 3786
Db 4200 TTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCAGCTTAAAGGATTTGGTCAATG 4142
Qy 3787 AGATTTATGTGACCAACAAACGGCCATCGTGCTCCCACTCTGTGAGTTCCGGGGCATATG 3846
Db 4141 ----- 4142
Qy 3847 ATGCGCGATAGCCGCTGCTGTTTCTGATGCCAGATTTGCACTGCCGGTAGAAC 3906
Db 4141 ----- 4142
Qy 3907 TCCGCGAGTGTCTCAGCTCAGCGACGAGCTGAACCAACTCCGCGAGGGATTCGAGCCG 3966
Db 4141 -----GCCCG 4137
Qy 3967 GGGTGGCGGAAGAACTCCAGCATGATATCCCGGCTGGAGAGATCATCCAGCCGCGTCC 4026
Db 4136 GGGTGGCGGAAGAACTCCAGCATGATATCCCGGCTGGAGAGATCATCCAGCCGCGTCC 4077
Qy 4027 CGAAAAACGATTTCCGAAGCCCAACCTTTCATAGAAGCGGGGTGGAATTCGAAATCTCGT 4086
Db 4076 CGAAAAACGATTTCCGAAGCCCAACCTTTCATAGAAGCGGGGTGGAATTCGAAATCTCGT 4017
Qy 4087 GATGGCAGTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4146
Db 4016 GATGGCAGTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3957
Qy 4147 ACTGCTCAAGAAAGCGCATATGAAGCGCATGCGCTCGCATATGGGAGCGCCATACCTTAA 4206
Db 3956 ACTGCTCAAGAAAGCGCATATGAAGCGCATGCGCTCGCATATGGGAGCGCCATACCTTAA 3897
Qy 4207 GCAAGAAAGCGCATATGAAGCGCATATGAAGCGCATATGAAGCGCATATGAAGCGCATATGAAG 4266
Db 3896 GCAAGAAAGCGCATATGAAGCGCATATGAAGCGCATATGAAGCGCATATGAAGCGCATATGAAG 3837
Qy 4267 ACCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCGCCACAGTGCATGATACAGAAA 4326
Db 3836 ACCTATGCTCTGATAGCGGTCCGCCACACCCAGCCGCGCCACAGTGCATGATACAGAAA 3777
Qy 4327 AGCGCCATTTTCCACCATGATATTTCCGCAAGCAGCGCATGCGCATGCGCATGCGCATGCGCAT 4386
Db 3776 AGCGCCATTTTCCACCATGATATTTCCGCAAGCAGCGCATGCGCATGCGCATGCGCATGCGCAT 3717
Qy 4387 CCTGCGCGTCCGCGCATGCGCGCTTGAAGCTGCGGAAAGTTGGGCTGGCGCGAGCCCT 4446
Db 3716 CCTGCGCGTCCGCGCATGCGCGCTTGAAGCTGCGGAAAGTTGGGCTGGCGCGAGCCCT 3657
Qy 4447 GATGCTTTTGTCCAGATCATCTGATGCAAGACCGGCTTTCATCCGATGAGTGTCTC 4506
Db 3656 GATGCTTTTGTCCAGATCATCTGATGCAAGACCGGCTTTCATCCGATGAGTGTCTC 3597
Qy 4507 GCTGATGCGATTTTGTGCTTGGTGTGCAAGTGGGCAAGTACCGGATCAAGCGTATGCA 4566
Db 3596 GCTGATGCGATTTTGTGCTTGGTGTGCAAGTGGGCAAGTACCGGATCAAGCGTATGCA 3537
Qy 4567 GCGCGCGCATTTGATTCAGCGATGATGATATCTTCTCGGCGAGGCAAGGATGATGCA 4626
Db 3536 GCGCGCGCATTTGATTCAGCGATGATGATATCTTCTCGGCGAGGCAAGGATGATGCA 3477
Qy 4627 GGAAGTCTGCCCCCGGCACTTCCGCAATATGACGAGCTTCTCCGCTTCACTGATGCA 4686
Db 3476 GGAAGTCTGCCCCCGGCACTTCCGCAATATGACGAGCACTTCTCCGCTTCACTGATGCA 3417
Qy 4687 GCTGAGCAAGCTGCGCAAGAAAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4746
Db 3416 GCTGAGCAAGCTGCGCAAGAAAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3357
Qy 4747 GCTGCTGCAATTCATGAGGCAACCGGACAGTCTGCTTGAACAAAAAGAACCGGCGCC 4806

Db 2706 GGGGCTTCTCAATGCTCAGCGCTGAGTATCTCAGTTGCGTGGTGGTGGCTCCAA 2765
Qy 3366 GCTGGGCTGTGTGACGAAACCCCGCTTACGCCCGACCGGTGGCTTATCCGGTAACTA 3425
Db 2766 GCTGGGCTGTGTGACGAAACCCCGCTTACGCCCGACCGGTGGCTTATCCGGTAACTA 2825
Qy 3426 TCGCTTGAATCCAAACCCCGGTAAAGACGACTTATCGCCACTGGACAGACCACTGGTAA 3485
Db 2826 TCGCTTGAATCCAAACCCCGGTAAAGACGACTTATCGCCACTGGACAGACCACTGGTAA 2885
Qy 3486 CAGGATTAGACAGACGAGTATGAGCGGTGCTACAGAGTCTTGAAGTGTGGCTTAA 3545
Db 2886 CAGGATTAGACAGACGAGTATGAGCGGTGCTACAGAGTCTTGAAGTGTGGCTTAA 2945
Qy 3546 CTACGGCTACCTAGAAAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
Db 2946 CTACGGCTACCTAGAAAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT 3005
Qy 3606 CGGAAAAAGAGTGTGATGCTCTTGAATCGGCAAAACCAACCGCTGTAGCGGTGGTTT 3665
Db 3006 CGGAAAAAGAGTGTGATGCTCTTGAATCGGCAAAACCAACCGCTGTAGCGGTGGTTT 3065
Qy 3666 TTTTGTGACAGACGAGATTAACGCGCAAAAAAAGATCTCAAGAAAGTCTTTGAT 3725
Db 3066 TTTTGTGACAGACGAGATTAACGCGCAAAAAAAGATCTCAAGAAAGTCTTTGAT 3125
Qy 3726 CTTTTCTACGCGGCTCTGACGCTCAGTGAACGAAAACTCAGTTAAGGAAATTTTGTCTAT 3785
Db 3126 CTTTTCTACGCGGCTCTGACGCTCAGTGAACGAAAACTCAGTTAAGGAAATTTTGTCTAT 3185
Qy 3786 GAGATTATCGTCGACCAAGGCGCATCTGTGCTCCCACTCCTGCAAGTTGCGGGGCGATG 3845
Db 3186 GAG----- 3188
Qy 3846 GATGCGGAGATAGCCGCTGCTGTTCTTGATGTCGACGGAATTTGCACTGCCGTAGAA 3905
Db 3189 ----- 3188
Qy 3906 CTCGCCGAGGTCGTCACGCTCAGGCGACAGCTGAACCACTGCCGAGGGGATGAGCCC 3965
Db 3189 -----CGATACATATTTGATGATTTGAAAAATTAACCAATAG 3229
Qy 3966 GGGGTGGCGAAGAACTCAAGCATGAGATCCCGCGCTGAGAGATCATCAGCCGCGCTC 4025
Db 3230 GGGTTCGCGGCACTTTCGCCGAAAGTGCCACTGTATGCGGTGAATACCGCACAG 3289
Qy 4026 CCGAAAAAGATTCGGAAGCCCACTTTCAATAGAGCGCGGTGAATCGAAATCTCG 4085
Db 3290 ATGGGTAAAGGAAAAATACCGCATCAGAAATTGTAAAGCGTTAATAAT----- 3337
Qy 4086 TGATGCAAGTTGGGCGCTCGCTTGTGTGCTATTTCAACCCAGAGTCCCGCTCAGAG 4145
Db 3338 -----TCAGAG 3344
Qy 4146 AACTCGTCAAGAAAGCGATGAGAGCGATGCGCTGCGAATCGGAGCGCGATCCGTAA 4205
Db 3345 AACTCGTCAAGAAAGCGATGAGAGCGATGCGCTGCGAATCGGAGCGCGATCCGTAA 3404
Qy 4206 AGCAGAGAAAGCGGTGAGCCCATTTGCGCGCAAGCTTTCAAGCAATATCACGGTTAGCC 4265
Db 3405 AGCAGAGAAAGCGGTGAGCCCATTTGCGCGCAAGCTTTCAAGCAATATCACGGTTAGCC 3464
Qy 4266 AAGCGTATGTCTGATAGCGGTCCGCAACCCGAGCGGCGCAAGTGTGAATCCGAA 4325
Db 3465 AAGCGTATGTCTGATAGCGGTCCGCAACCCGAGCGGCGCAAGTGTGAATCCGAA 3524
Qy 4326 AAGCGGCAATTTTCCACATGATATTTGCGCAAGAGGAGCATGCGATGGTCAAGACAGA 4385
Db 3525 AAGCGGCAATTTTCCACATGATATTTGCGCAAGAGGAGCATGCGATGGTCAAGACAGA 3584
Qy 4386 TCCTGCGGTGCGGATGCGGCGCTTGAAGCTGCGAAACAGTTGAGTGGCGCGAGCCCC 4445

Db 3585 TCCTGCGGTGCGGAGCATGCTCGCTTGAAGCTTGGCGAAGAGTTGCGGCGCGAGCCCC 3644
Qy 4446 TGATGCTCTTTCGTCAGATCATCTGATGACAAAGCCGCTTCCATCCGAGTACGTGCT 4505
Db 3645 TGATGCTCTTTCGTCAGATCATCTGATGACAAAGCCGCTTCCATCCGAGTACGTGCT 3704
Qy 4506 CGCTGATGAGATGTTTGGCTTGTGTGGAATGGGACAGTGAAGCCGATCAAGCGTATGC 4565
Db 3705 CGCTGATGAGATGTTTGGCTTGTGTGGAATGGGACAGTGAAGCCGATCAAGCGTATGC 3764
Qy 4566 AGCCGCGCATTTGATCAGACCATGATGATPACTTTCTGCGCAGAGCAAGTGAATGAC 4625
Db 3765 AGCCGCGCATTTGATCAGACCATGATGATPACTTTCTGCGCAGAGCAAGTGAATGAC 3824
Qy 4626 AGGAGATCTTGGCCCCGCACTTGGCCCATAGACGACATCTTCCCTCCGCTTACGTGACA 4685
Db 3825 AGGAGATCTTGGCCCCGCACTTGGCCCATAGACGACATCTTCCCTCCGCTTACGTGACA 3884
Qy 4686 AGGTGAGACAGACTGCGCAAGGAAAGCCCGTGTGGCCAGCCAGATAGCCGCTGACC 4745
Db 3885 AGGTGAGACAGACTGCGCAAGGAAAGCCCGTGTGGCCAGCCAGATAGCCGCTGACC 3944
Qy 4746 TCGTCTTGAAGTTCAATTCAGGGGCAACGAGTGGTCTTGAACAAAAAGAACCGGAGCGC 4805
Db 3945 TCGTCTTGAAGTTCAATTCAGGGGCAACGAGTGGTCTTGAACAAAAAGAACCGGAGCGC 4004
Qy 4806 CCTGCGCTGACAGCCGGAACAGGCGGATCAGACAGCCATTTGTGTGTGCGCCAG 4865
Db 4005 CCTGCGCTGACAGCCGGAACAGGCGGATCAGACAGCCATTTGTGTGTGCGCCAG 4064
Qy 4866 TCATAGCCGAATAGCTCTTCCACCCCAAGCGGCGGAGAACTGTGCAATCCATCTTGT 4925
Db 4065 TCATAGCCGAATAGCTCTTCCACCCCAAGCGGCGGAGAACTGTGCAATCCATCTTGT 4124
Qy 4926 TCATATATGGAAGAGATCTCATCTGTCTTGTATCATGATCTTGAATCCCTGCGCAT 4985
Db 4125 TCATATATGGAAGAGATCTCATCTGTCTTGTATCATGATCTTGAATCCCTGCGCAT 4184
Qy 4986 CAG 4988
Db 4185 CAG 4187

RESULT 7
US-10-811-028A-2
; Sequence 2, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Jui
; APPLICANT: Genetec, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811, 028A
; PRIOR FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US 60/458, 793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4293
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pMB1-HAMMSOD
; OTHER INFORMATION: plasmid expression vector
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1940)
; OTHER INFORMATION: n = g, a, c or t
US-10-811-028A-2
Query Match 32.1%; Score 1697.8; DB 8; Length 4293;

Best Local Similarity 86.7%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;

Qy 2706 CTAGACGATATCATGTCATAGCTGTTTCCGTGNGAATTTGTTATCCGCTCACAATTC 2765
Db 2212 CTGGCGATATCATGTCATAGCTGTTTCCGTGNGAATTTGTTATCCGCTCACAATTC 2271
Qy 2766 AACACATATCAGAGCCGGAAGATTAAGTGTAAACCTCGGGGTGCTTAATAGTAGCTA 2825
Db 2272 AACACATATCAGAGCCGGAAGATTAAGTGTAAACCTCGGGGTGCTTAATAGTAGCTA 2331
Qy 2826 ACTCATTAATTTGGTTGGCTCATCTGCGCTTTCCAGTGGGAAAACCTGTCTGCA 2885
Db 2332 ACTCATTAATTTGGTTGGCTCATCTGCGCTTTCCAGTGGGAAAACCTGTCTGCA 2391
Qy 2886 GCTGATTAATGAATCGGCAACCGCGGGGAGAGCGGTTTGCCTATTTGGGCGCTCTC 2945
Db 2392 GCTGATTAATGAATCGGCAACCGCGGGGAGAGCGGTTTGCCTATTTGGGCGCTCTC 2451
Qy 2946 CGCTTCTCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3005
Db 2452 CGCTTCTCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2511
Qy 3006 TCACCTCAAGCGGCTAATACGTTATCCACAGAAATCAGGGGATTAACGAGAAAGAAAT 3065
Db 2512 TCACCTCAAGCGGCTAATACGTTATCCACAGAAATCAGGGGATTAACGAGAAAGAAAT 2571
Qy 3066 GTGAGCAAAAGGCGCAAGAAAGCCGTAACCCGTAACCCGCTGCTGCTGCTGCTGCT 3125
Db 2572 GTGAGCAAAAGGCGCAAGAAAGCCGTAACCCGTAACCCGCTGCTGCTGCTGCTGCT 2631
Qy 3126 CCATAGGCTCGGCGCCCTGACAGCATCACAAAATGAGCGCTCAAGTCAAGAGTGGCG 3185
Db 2632 CCATAGGCTCGGCGCCCTGACAGCATCACAAAATGAGCGCTCAAGTCAAGAGTGGCG 2691
Qy 3186 AAACCCGACAGAGCTATTAAGATACAGAGCGTTTCCCTGAAAGCTCCCTGAGCGTC 3245
Db 2692 AAACCCGACAGAGCTATTAAGATACAGAGCGTTTCCCTGAAAGCTCCCTGAGCGTC 2751
Qy 3246 TCCCTGTTCCGACCTTCCGCTTACCGGATACCTGCTGCTGCTGCTGCTGCTGCTGCT 3305
Db 2752 TCCCTGTTCCGACCTTCCGCTTACCGGATACCTGCTGCTGCTGCTGCTGCTGCTGCT 2811
Qy 3306 GAGCGCTTCTCATAGCTCAGCGCTGAGGATCTCAGTTGAGTGGTGGTCCCTCAA 3365
Db 2812 GAGCGCTTCTCATAGCTCAGCGCTGAGGATCTCAGTTGAGTGGTGGTCCCTCAA 2871
Qy 3366 GCTGGGCTGTGTGACGAAACCCCGCTTCAAGCCGACCGCTGCTGCTGCTGCTGCTGCT 3425
Db 2872 GCTGGGCTGTGTGACGAAACCCCGCTTCAAGCCGACCGCTGCTGCTGCTGCTGCTGCT 2931
Qy 3426 TCGCTTGAATCCGACCCCGGTAAACAGACTTAATCCGCACTGCAAGGCACTGGTAA 3485
Db 2932 TCGCTTGAATCCGACCCCGGTAAACAGACTTAATCCGCACTGCAAGGCACTGGTAA 2991
Qy 3486 CAGGATTAAGCAGAGCGATTAAGGCGGTGCTAAGAGTCTTGAAGTGGTGGCTTAA 3545
Db 2992 CAGGATTAAGCAGAGCGATTAAGGCGGTGCTAAGAGTCTTGAAGTGGTGGCTTAA 3051
Qy 3546 CTACGGCTACCTAAGAAACAGATTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3605
Db 3052 CTACGGCTACCTAAGAAACAGATTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3111
Qy 3606 CGGAAAAAGAGTGTGTGCTTTGATCTGCGCAAAACACCGCTGGTAGCGGTGTTT 3665
Db 3112 CGGAAAAAGAGTGTGTGCTTTGATCTGCGCAAAACACCGCTGGTAGCGGTGTTT 3171
Qy 3666 TTTTGTTCAGAGCAGATTAAGCGCAAAAGAGTCTTGAAGTGGTGGCTTAA 3725
Db 3172 TTTTGTTCAGAGCAGATTAAGCGCAAAAGAGTCTTGAAGTGGTGGCTTAA 3231
Qy 3726 CTTTTCAGAGGCTCTGACGCTCAGTGAACGAAACTCAGTTAAGGATTTTGTCTAT 3785
Db 3232 CTTTTCAGAGGCTCTGACGCTCAGTGAACGAAACTCAGTTAAGGATTTTGTCTAT 3291

Qy 3786 GAGATTAATCTGACCAAAAGCGGCATCTGTGCTCCCACTCTCGAGTTGGGGGCAATG 3845
Db 3292 GAG----- 3294
Qy 3846 GATGCGGATAGCCGCTGCTGTTCTCTGATGCCAGATTTGCACTGCCGTAGAA 3905
Db 3295 ----- 3294
Qy 3906 CTCGCCAGATCTGTCAGAGCTCAGGCAAGCTGAACCACTCCGAGGGGATGAGCCC 3965
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Qy 3966 GGGTGGGCGGAAGAACTCCAGCATGATCCCGCGCTGAGGATTCATCCAGCCGGGCTC 4025
Db 3336 GGGTGGGCGGAAGAACTCCAGCATGATCCCGCGCTGAGGATTCATCCAGCCGGGCTC 3395
Qy 4026 CCGAAAAAGATTCGAAAGCCCACTTTCAATAGAAAGCGCGGTGGAATGAAATCTCG 4085
Db 3395 ----- 3443
Qy 4086 TGATGCAAGTTGGGCGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4145
Db 3444 ----- 3450
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Qy 4206 AGCAGAGAAAGCGGTGAGGCGATTCGCGCGCAAGCTCTTCAAGATATCAAGGTTAGCC 4265
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Qy 4266 AAGCTATGTCCTGATAGCGGTGCGCCACACCGAGCGGCGCAAGTGAATCCAGAA 4325
Db 3571 AAGCTATGTCCTGATAGCGGTGCGCCACACCGAGCGGCGCAAGTGAATCCAGAA 3630
Qy 4326 AAGGCGCATTTTTCACATGATTAATTTGGCAAGGAGCATTCGCTGCTGCTGCTGCT 4385
Db 3631 AAGGCGCATTTTTCACATGATTAATTTGGCAAGGAGCATTCGCTGCTGCTGCTGCTGCT 3690
Qy 4386 TCCCTGCGCTGCGGCAAGCGGCTTGAAGCTGGCGCAAGTTCGCTGCTGCTGCTGCTGCT 4445
Db 3691 TCCCTGCGCTGCGGCAAGCGGCTTGAAGCTGGCGCAAGTTCGCTGCTGCTGCTGCTGCT 3750
Qy 4446 TGAATGCTCTTCTGTCAGATCATCTGATTCGACAAAGCCGCTTCCATCCGATGCTGCT 4505
Db 3751 TGAATGCTCTTCTGTCAGATCATCTGATTCGACAAAGCCGCTTCCATCCGATGCTGCT 3810
Qy 4506 CGCTCGATGCGATGTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4565
Db 3811 CGCTCGATGCGATGTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3870
Qy 4566 AGCGCGCGCATTCGATCAGCATGATGATGATCTTCTCGGCAAGGAGCAAGTGAAGTAC 4625
Db 3871 AGCGCGCGCATTCGATCAGCATGATGATGATCTTCTCGGCAAGGAGCAAGTGAAGTAC 3930
Qy 4626 AGGAGATCTGCGCCCGGCACTTCCGCAATAGAGCCAGTCCCTTCCGCTTCAAGTACA 4685
Db 3931 AGGAGATCTGCGCCCGGCACTTCCGCAATAGAGCCAGTCCCTTCCGCTTCAAGTACA 3990
Qy 4686 AGCTGAGCAGAGCTGCGCAAGAAAGCCCGTGTGCGCAGCCAGCATCCGCGTGGC 4745
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Db 4051 TCGTCTGCGAGTTCATTCAGGCGGCAAGGATCGCTTTCGCAAAAGAAACCGGGCGC 4110
Qy 4806 CCGTGGCGTGAAGCGCGGAAACAGGCGGCTCAGAGAGCGGATGCTGTTGCTGCGCAG 4865
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QY 4866 TCATAGCGAATAGCTCTCCACCCAGGCGCGAGAAACCTGCGTCAATCCATCTTGT 4925
DB 4171 TCATAGCGAATAGCTCTCCACCCAGGCGCGAGAAACCTGCGTCAATCCATCTTGT 4230
QY 4926 TCATCATTCGGAACGATCTCTCATCTCTCTCTTGTATCAGATCTTGTATCCCTGCGCAT 4985
DB 4231 TCATCATTCGGAACGATCTCTCATCTCTCTCTTGTATCAGATCTTGTATCCCTGCGCAT 4290
QY 4986 CAG 4988
DB 4291 CAG 4293

RESULT 8
US-10-811-028A-1
Sequence 1, Application US/10811028A
Publication No. US20050043258A1
GENERAL INFORMATION:
APPLICANT: Bennett, Michael
APPLICANT: Chen, Yen-Ju
APPLICANT: Genetec, Inc.
TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
FILE REFERENCE: 020714-002410US
CURRENT FILING DATE: 2004-03-25
PRIORITY FILING DATE: 2004-03-25
PRIORITY FILING DATE: 2003-03-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 4332
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: pMB1-MhSOD
OTHER INFORMATION: plasmid expression vector
NAME/KEY: modified_base
LOCATION: (1979)
OTHER INFORMATION: n = g, a, c or t
US-10-811-028A-1

Query Match 32.1%; Score 1697.8; DB 8; Length 4332;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;

QY 2706 CTAGACGTATCATGTCATAGCTGTTTCTGTGTAAATTGTTATCCGCTCACAATTCC 2765
DB 2251 CTGGCGTAAATCATGTCATAGCTGTTTCTGTGTAAATTGTTATCCGCTCACAATTCC 2310
QY 2766 ACACAATCATGAGCGGAGGAGCATTAAGTGAAGAGCTGGGGAGCTTAATGAGAGAGCTA 2825
DB 2311 ACACAAATCATGAGCGGAGGAGCATTAAGTGAAGAGCTGGGGAGCTTAATGAGAGAGCTA 2370
QY 2826 ACTCACATTAATGCTGTTGCGCTCACTGCGCTTTTCAGTCCGGAACCTGTGTCGCA 2885
DB 2371 ACTCACATTAATGCTGTTGCGCTCACTGCGCTTTTCAGTCCGGAACCTGTGTCGCA 2430
QY 2886 GCTGCTATTAATGATCGGCGCAAGCGCGGGAGAGGCGTTTGGCTATTTGGCGCTTTTC 2945
DB 2431 GCTGCTATTAATGATCGGCGCAAGCGCGGGAGAGGCGTTTGGCTATTTGGCGCTTTTC 2490
QY 2946 CGCTTCTGCTCACTGACTCGCTGCGCTCGGTGCTTGGCTGCGGAGCGGATCAGC 3005
DB 2491 CGCTTCTGCTCACTGACTCGCTGCGCTCGGTGCTTGGCTGCGGAGCGGATCAGC 2550
QY 3006 TCATCTAAAGCGGTAATACGTTATCAGAGATCAGGAGATTAACGAGAAAGAAAT 3065
DB 2551 TCATCTAAAGCGGTAATACGTTATCAGAGATCAGGAGATTAACGAGAAAGAAAT 2610
QY 3066 GTGAGCAAAAGGCGAGCAAAAGGCGAGAAACCTTAAGAGCGCGCTTGGCTGCTTTT 3125

DB 2611 GTGAGCAAAAGGCGAGCAAAAGGCGAGAAACCTTAAGAGCGCGCTTGGCTGCTTTT 2670
QY 3126 CCATAGGCTCCGCGCCCTGAGAGAGATCAAAAATTCAGCGCTCAGAGTGGGCG 3185
DB 2671 CCATAGGCTCCGCGCCCTGAGAGAGATCAAAAATTCAGCGCTCAGAGTGGGCG 2730
QY 3186 AAACCCGACAGAGCTTAAGATACAGAGGCTTTCCCTGGAAGCTCCTCGTGCGTC 3245
DB 2731 AAACCCGACAGAGCTTAAGATACAGAGGCTTTCCCTGGAAGCTCCTCGTGCGTC 2790
QY 3246 TCCGTTCGAGCCCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTGGAAGCGT 3305
DB 2791 TCCGTTCGAGCCCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTGGAAGCGT 2850
QY 3306 GCGCTTTCATAGCTACGCTGATGATATCATGTTGGGTAGTGGTTCGCTCA 3365
DB 2851 GCGCTTTCATAGCTACGCTGATGATATCATGTTGGGTAGTGGTTCGCTCA 2910
QY 3366 GCTGAGCTGTGTCAGAAACCCCGCTTACGCGGAGCGCGTGCCTTATCCGTA 3425
DB 2911 GCTGAGCTGTGTCAGAAACCCCGCTTACGCGGAGCGCGTGCCTTATCCGTA 2970
QY 3426 TCGTCTTGAATCCAAACCCGTAAGACAGACTTATCGCACTGCGAGCCACTGTA 3485
DB 2971 TCGTCTTGAATCCAAACCCGTAAGACAGACTTATCGCACTGCGAGCCACTGTA 3030
QY 3486 CAGATTAGCAGAGGATATGATAGCGGTGCTACAGATTCTTGAAGTGGGCTTA 3545
DB 3031 CAGATTAGCAGAGGATATGATAGCGGTGCTACAGATTCTTGAAGTGGGCTTA 3090
QY 3546 CTACGCTACACTAGAAAGACAGTATTTGATCTGCGCTCTGCTGAGCACTTA 3605
DB 3091 CTACGCTACACTAGAAAGACAGTATTTGATCTGCGCTCTGCTGAGCACTTA 3150
QY 3606 CGGAAAAAGATTGTAGCTCTTGAATCCGCAAAACCAACCGCTGTAGCGGTGTT 3665
DB 3151 CGGAAAAAGATTGTAGCTCTTGAATCCGCAAAACCAACCGCTGTAGCGGTGTT 3210
QY 3666 TTTTGTTCAGACAGACAGATTACGCGAGAAAAAAGATCTCAGAGATCTTGTAT 3725
DB 3211 TTTTGTTCAGACAGACAGATTACGCGAGAAAAAAGATCTCAGAGATCTTGTAT 3270
QY 3726 CTTTTCTACGGGTCTGACGCTCAGTGAACGAAACCTCAGTTAAGGATTTGTCTAT 3785
DB 3271 CTTTTCTACGGGTCTGACGCTCAGTGAACGAAACCTCAGTTAAGGATTTGTCTAT 3330
QY 3786 GAGATTATGTGACCAAAAGCGGCTGCTCCCACTCCTGCACTTGGGGGAGATG 3845
DB 3331 GAG----- 3333
QY 3846 GATGCGGATAGCGCTGCTGTTTCTGATGCGGAGATTGCACTGCGGTAAGA 3905
DB 3334 ----- 3333
QY 3906 CTCGCGAGGTGCTCAGGCTCAGGAGAGCTGAACAACTCGCGAGGGATCGAGCC 3965
DB 3334 ----- 3374
QY 3966 GGGGTGGGAGAAATCTCAGAGATGATCCCGGCTGGAAGATATCAGCGCGGCTC 4025
DB 3375 GGGGTGGGAGCAATTTCCCGAAAGTGCACTGTATGCGGTGAAATACCGGACAG 3434
QY 4026 CCGAAGAGATTCGAGAGCCCACTTTCATAGAGGCGGAGTGAATCGAAATCTCG 4085
DB 3435 ATGCGTAAGAGAAATACCGCATCAGAAATTTGTAAGGCTTAATAT----- 3482
QY 4086 TGATGCAAGTTGGGCGTGTGCTGCTGATTTGAAACCCGAGATCCGCTCAGAG 4145
DB 3483 -----TCGAGAG 3489
QY 4146 AACTGCTCAAGAGGAGATGAGAGGAGATGCGCTGCGATTCGGAGCGCGGATACCTGA 4205
DB 3490 AACTGCTCAAGAGGAGATGAGAGGAGATGCGCTGCGATTCGGAGCGCGGATACCTGA 3549

QY 3606 CGGAAAAAGATTGTAGCTTTGATCCGCGCAACAAACCAACCGCTGTAGCGGTGTTT 3665
DB 4572 CGGAAAAAGATTGTAGCTTTGATCCGCGCAACAAACCAACCGCTGTAGCGGTGTTT 4631
QY 3666 TTTTGTTCGAAAGCAGCATTTACGCGCAGAAAAAGATCTTCAGAAAGATCTTTGAT 3725
DB 4632 TTTTGTTCGAAAGCAGCATTTACGCGCAGAAAAAGATCTTCAGAAAGATCTTTGAT 4691
QY 3726 CTTTTCATCGGGGTCTGACGTCTGAGTGAACGAAACTCACGTTAAGGATTTTGTGAT 3785
DB 4692 CTTTTCATCGGGGTCTGACGTCTGAGTGAACGAAACTCACGTTAAGGATTTTGTGAT 4751
QY 3786 GAGATTATCGTCGACCAAGCGCCATCGTGCCTCCCACTCTCGAGTTCCGGGGGATG 3845
DB 4752 GAG----- 4754
QY 3846 GATGCGGGAATGACCGCTGCTGTTTCTGTGATGCCAGCGATTTCAGCTGCCGATGAA 3905
DB 4755 ----- 4754
QY 3906 CTCGCGAGGTCCTGACGCTCAGGCGACGCTGAACCACTGCCGAGGGATCGAGCCC 3965
DB 4755 -----CGATACATATTGTAATGATTTAGAAAAATTAACAAATAG 4795
QY 3966 GGGGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGAGAGATTCAGCGCGCTC 4025
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QY 4026 CCGGAAAAAGATTCGGAAGCCCACTTTTATAGAGCGCGGTGGAATCGAAATCTCG 4085
DB 4856 ATGCGTAAAGAGAAAAATACCGCATCAGAAATTTGTAACGTTAATAT----- 4903
QY 4086 TGATGGCAGGTGGGCGTCTGTGTGATTTGCAACCCAGAGTCCCGCTCAGAG 4145
DB 4904 -----TCAGAG 4910
QY 4146 AACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTGCGAATCGGAGCGCGATACCGTAA 4205
DB 4911 AACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTGCGAATCGGAGCGCGATACCGTAA 4970
QY 4206 AGCAGAGAAAGCGGTGACGCCCATTCGCGCCGCAAGCTTTCAGCAATATCACGGTAGCC 4285
DB 4971 AGCAGAGAAAGCGGTGACGCCCATTCGCGCCGCAAGCTTTCAGCAATATCACGGTAGCC 5030
QY 4266 AAGCGTATGCTGATAGCGGTGCGGCAACCGCGCGCGCAAGTGAATCCAGAA 4325
DB 5031 AAGCGTATGCTGATAGCGGTGCGGCAACCGCGCGCGCAAGTGAATCCAGAA 5090
QY 4326 AAGCGCGCATTTTCCACCATGATATTCGCGCAAGAGGATTCGCATGGGTACGACGAGA 4385
DB 5091 AAGCGCGCATTTTCCACCATGATATTCGCGCAAGAGGATTCGCATGGGTACGACGAGA 5150
QY 4386 TCTTCGCGGTGCGGCAATGCGCGCTTGAAGCTTGCGCAACAGTTGCGCTGCGCGAGCCC 4445
DB 5151 TCTTCGCGGTGCGGCAATGCGCGCTTGAAGCTTGCGCAACAGTTGCGCTGCGCGAGCCC 5210
QY 4446 TGATGCTCTTGTGTCAGATTCCTGATCGACAGACCGGCTTCATCCGAGTACGTCGCT 4505
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QY 4506 CGCTCGATGCGATTTTCGCTTGTGTGTCGATGGGCGAGGTAGCCGATCAAGCGTATGC 4565
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QY 4566 AGCGCGCGCATTTGATCAGCATGATGATGATCTTTCTTCGCGAGAGCAAGGTGATGAC 4625
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QY 4626 AGGAGATCTGCGCGCGCACTTGGCCAAATAGCAGCAGTCCCTTCGCGCTTCAGTACA 4685
DB 5391 AGGAGATCTGCGCGCGCACTTGGCCAAATAGCAGCAGTCCCTTCGCGCTTCAGTACA 5450

QY 4686 ACGTCGAGCAGACGTCGCGAAGGAACGCCCGTGTGTGGCCAGCCACGATAGCCGCTGCC 4745
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QY 4746 TCGTCTGCAAGTTTCAATTCAGGGGCAACCGGACAGGTGCGTCTTGAACAAAAGAACCGGGCG 4805
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QY 4806 CCGTGGCTGACGACCGCGGAACACGGGGGATCAGACACCGCATTTGCTGTTGGCCAG 4865
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DB 5631 TCATAGCCGAATAGCTCTCCACCCAGCGCGCGGAGAACTGCGTGAATCATCTTGT 5690
QY 4926 TCATATGCGAAGAACGATCTCTCATCTGTCTTGTATCAGATTTGATCCCTGCGCCAT 4985
DB 5691 TCATATGCGAAGAACGATCTCTCATCTGTCTTGTATCAGAGCTTGATCCCTGCGCCAT 5750
QY 4986 CAG 4988
DB 5751 CAG 5753

RESULT 10
US-10-811-028A-4
; Sequence 4, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Generic, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US 60/458,793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5760
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pMB1-Mt-CAT
; OTHER INFORMATION: Plasmid expression vector
; US-10-811-028A-4

Query Match 32.1%; Score 1697.8; DB 8; Length 5760;
Best local Similarity 86.7%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;
QY 2706 CTNAGCGTAATCATGCTGATAGCTGTTTCTGTGTGAATTTGTTATCCGCTCAATTC 2765
DB 3679 CTGCGGTAATCATGCTGATAGCTGTTTCTGTGTGAATTTGTTATCCGCTCAATTC 3738
QY 2766 ACACAATATACGAGCGCGGAAGCAATAAGTAAAGCTGGGGGCTTAATGATGAGCTTA 2825
DB 3739 ACACAATATACGAGCGCGGAAGCAATAAGTAAAGCTGGGGGCTTAATGATGAGCTTA 3798
QY 2826 ACTCACATTAATTTGCTGTGCTCACTGCGCGCTTTTCAGTCGGGAACCTGTGTCGCA 2885
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QY 2946 CGCTTCCTGCTCACTGACCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3005
DB 3919 CGCTTCCTGCTCACTGACCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3978

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Db 3979 TCACCTCAAAAGCGGTATATCGGTTATCCACAGAAATCAGGGATTAACGAGAAAAGAAATCAT 4038
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QY 3066 GTGAGCAAAAGCGGACGCAAAAGCGGAGAACCGTAAAAAGCCGGCTTGTGGCGCTTTT 3125
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Db 4459 CAGGATTAAGCAGACCGAGATATGTAGGGGGTCTACAGAGTTCTTGAAGTGTGGCTTAA 4518
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Db 4699 CTTTCTACGAGGCTGTAGCGCTCAGTGAACGAAACCTCACTTAAGGGATTTTGTGCAT 4758
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QY 4326 AAGCGGCATTTTTCACCATGATATTTGGGAAAGAGGATTCGCATGAGTACAGAGAA 4385
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| | | | |
QY 4386 TCTTCGCGCTCGGACATGCGCGCTTGAAGCTGTGCGAAACATTTGCTGCGCGAGCCC 4445
| | | | |
Db 5158 TCTTCGCGCTCGGACATGCGCGCTTGAAGCTGTGCGAAACATTTGCTGCGCGAGCCC 5217
| | | | |
QY 4446 TGATGCTCTTGTCTCAGATCATCTGATCGAACAAAGACCGGCTTCATCCGAGTACGTGCT 4505
| | | | |
Db 5218 TGATGCTCTTGTCTCAGATCATCTGATCGAACAAAGACCGGCTTCATCCGAGTACGTGCT 5277
| | | | |
QY 4506 CGCTCAGTGCAGATGTTTTCGCTTGTGTGTCGAATGGGCGAGTACCGGATCAAGCTATGC 4565
| | | | |
Db 5278 CGCTCAGTGCAGATGTTTTCGCTTGTGTGTCGAATGGGCGAGTACCGGATCAAGCTATGC 5337
| | | | |
QY 4566 AGCCCGCGCATTTGATATGACCATGATGATATCTTTCTCGCAGAGACGAAGTGAATGAC 4625
| | | | |
Db 5338 AGCCCGCGCATTTGATATGACCATGATGATATCTTTCTCGCAGAGACGAAGTGAATGAC 5397
| | | | |
QY 4626 AGGAGATCTGCGCCCGGACCTTGCGCCCAATAGACAGACGTCCTTCCGCTTACGTAGCA 4685
| | | | |
Db 5398 AGGAGATCTGCGCCCGGACCTTGCGCCCAATAGACAGACGTCCTTCCGCTTACGTAGCA 5457
| | | | |
QY 4686 ACCTGACGACAGCTGCGCAAGAAACGCGCTGTGTGCGACGACGATAGCCGCTGCC 4745
| | | | |
Db 5458 ACCTGACGACAGCTGCGCAAGAAACGCGCTGTGTGCGACGACGATAGCCGCTGCC 5517
| | | | |
QY 4746 TCGTCTGCACTTCAATTCAGGGCACCGGACAGTGTCTTGAACAAAAAGAACCGGGCGC 4805
| | | | |
Db 5518 TCGTCTGCACTTCAATTCAGGGCACCGGACAGTGTGTCTTGAACAAAAAGAACCGGGCGC 5577
| | | | |
QY 4806 CCCGCGCTGACAGCGCGGAAACAGGGGCGATCAGAGACGCGATTTGTGTGCGCCAG 4865
| | | | |
Db 5578 CCCGCGCTGACAGCGCGGAAACAGGGGCGATCAGAGACGCGATTTGTGTGCGCCAG 5637
| | | | |
QY 4866 TCATAGCGAATAGCTCTTCCACCCCAAGCGGCGGAAACCTGCGTCATCTTGT 4925
| | | | |
Db 5638 TCATAGCGAATAGCTCTTCCACCCCAAGCGGCGGAAACCTGCGTCATCTTGT 5697
| | | | |
QY 4926 TCATATGCGAAGACGATCTCATCTGTCTTGAATCAGATTTGAATCCCTGCGCAT 4985
| | | | |
Db 5698 TCATATGCGAAGACGATCTCATCTGTCTTGAATCAGATTTGAATCCCTGCGCAT 5757
| | | | |
QY 4986 CAG 4988
| | | | |
Db 5758 CAG 5760
| | | | |

RESULT 11
US-10-286-186-16/c
; Sequence 16, Application US/10286186
; Publication No. US20030143741A1
; GENERAL INFORMATION:
; APPLICANT: PALMER, KENNETH E.
; APPLICANT: POGUE, GARY P.
; TITLE OF INVENTION: ROLLING CIRCLE REPLICON EXPRESSION

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; TITLE OF INVENTION: VECTOR
; FILE REFERENCE: 00801017900US00
; CURRENT APPLICATION NUMBER: US/10/286,186
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/505,477
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 5225
; TYPE: DNA
; ORGANISM: Porcine Circovirus
US-10-286-186-16

Query Match      32.0%; Score 1692.4; DB 6; Length 5225;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2087; Conservative 0; Mismatches 206; Indels 231; Gaps 4;

QY      2942 CTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGTTCGTTCCGCTCGCGGAGCGGTAT 3001
DB      5225 CTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGTTCGTTCCGCTCGCGGAGCGGTAT 5166
QY      3002 CAGTCTCAAGAGCGGTATACGGTTATTCAGAGATCAGGGGATTAACGAGAGAAAGA 3061
DB      5165 CAGTCTCAAGAGCGGTATACGGTTATTCAGAGATCAGGGGATTAACGAGAGAAAGA 5106
QY      3062 ACATGTAGCAAAAGGCGAGCAAAAGGCGAGAAACGGTAAAGGCGCGTGTGGCGT 3121
DB      5105 ACATGTAGCAAAAGGCGAGCAAAAGGCGAGAAACGGTAAAGGCGCGTGTGGCGT 5046
QY      3122 TTTTCCATAGAGCTCCGCCCTTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGT 3181
DB      5045 TTTTCCATAGAGCTCCGCCCTTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGT 4986
QY      3182 GGGCAAAACCGGACGAGCATATAAGATACCAAGGGGTTTCCCTCGAGAGCTCCTCGTGC 3241
DB      4985 GGGCAAAACCGGACGAGCATATAAGATACCAAGGGGTTTCCCTCGAGAGCTCCTCGTGC 4926
QY      3242 GCTCTCTGTTCCGACCGCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAA 3301
DB      4925 GCTCTCTGTTCCGACCGCTGCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAA 4866
QY      3302 GCGTGGCGCTTCTCATAGCTCAGCTGTAGATCTCAAGTCGGGTAGGTCGTTGCT 3361
DB      4865 GCGTGGCGCTTCTCATAGCTCAGCTGTAGATCTCAAGTCGGGTAGGTCGTTGCT 4806
QY      3362 CCAAGCTGGGCTGTGTGACGAAACCCCGCTTACGCCGACCGTGGCGCTTATCCGGTA 3421
DB      4805 CCAAGCTGGGCTGTGTGACGAAACCCCGCTTACGCCGACCGTGGCGCTTATCCGGTA 4746
QY      3422 ACTATCGTCTTGAAGTCCAAACCGGTAAGACAGCACTTATCGCCACTGGACAGCCACTG 3481
DB      4745 ACTATCGTCTTGAAGTCCAAACCGGTAAGACAGCACTTATCGCCACTGGACAGCCACTG 4686
QY      3482 GTAAACAGATTTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGATTCTTGAAGTGTGC 3541
DB      4685 GTAAACAGATTTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGATTCTTGAAGTGTGC 4626
QY      3542 CTAACTACGGCTACACTTAAGAAAGCACTATTTGGTATCTGGCTCTCTCTGAAGCACTTA 3601
DB      4625 CTAACTACGGCTACACTTAAGAAAGCACTATTTGGTATCTGGCTCTCTCTGAAGCACTTA 4566
QY      3602 CTTTCGAAAAAGATTGTAGTCTTGTATCCGGCAAAACCAACGCGTGTAGCGGTG 3661
DB      4565 CTTTCGAAAAAGATTGTAGTCTTGTATCCGGCAAAACCAACGCGTGTAGCGGTG 4506
QY      3662 GTTTTTTTGTTGCAAGCAGCATTAACGGCAGAAAAAAGATCTCAAGAGATCTT 3721
DB      4505 GTTTTTTTGTTGCAAGCAGCATTAACGGCAGAAAAAAGATCTCAAGAGATCTT 4446
QY      3722 TGATCTTTTCTAAGGGGTGTGACGCTCAGTGAACGAAAACTCAGTTAAGGATTTTGG 3781
DB      4445 TGATCTTTTCTAAGGGGTGTGACGCTCAGTGAACGAAAACTCAGTTAAGGATTTTGG 4386
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QY      3782 TCATGATATTATC----- 3794
DB      4385 TCATGATATTATCAAAAAGATCTTCACCTAATCCTTTAAATTAAATGAAGTTTA 4326
QY      3795 -----GTCGACCA 3802
DB      4325 GCACGTGATGTCCTGCTCTCGGCCACGAAAGTGCAGGATTCGCGCGCGGAGTCCGCA 4266
QY      3803 AAGCGGCATCTGCTCTCTCCCACTCTGTGAGTTCCGGGGCAATGATGCCGATAGCCGC 3862
DB      4265 GGGCGAACTCCCGCCCAAGGCTGCTCGCATCTCGGTATGCGCGGCGCGAGCGT 4206
QY      3863 TGCTGTTTCTGATAGTCGAGGATTTGCACTGCGGTGAGAACTCCGAGGATGCTGCA 3922
DB      4205 CCGGAAAGTTTGTGAGACGACCTCCGACCATTCGGCGTCAAGCTGTCCAGGCCGCGCA 4146
QY      3923 GCC----- 3925
DB      4145 CCACACCCAGGCGAGGGTGTGTCCGACCACTGTCCTGACCCGCTGATGAACA 4086
QY      3926 ----TCAGCAGCAGCTGAACCACTCGCAGGGGATTCAGCCCGGGGTGGGAGAACT 3982
DB      4085 GGGTCAGTCTGTCGGACCAACCGGCGAAGTCTCTCCAGAAATCCGGAGAACCC 4026
QY      3983 CCAGCATG-----AGATCCCGGCTGGAAGATCATCCAGCCGCGCTC 4025
DB      4025 CGAGCTGTGCAACTTGGCATGTGCGCTCTCACTGCTGCTATTAATTAAGCATTTATC 3966
QY      4026 CCGAAAAAGATTCGAGACCCCACTTTCATTAAGAAAGCGGCGGTGAATCGAATCTGC 4085
DB      3965 AGGTTATTGTCTCAAGCAGGATCATATTGAATGTATTGAATAAACAATAG 3906
QY      4086 TGATGCAAGTGTGGGCTGCTGTGTGCTGCTGCTTTCGAAACCCAGATCCCGC----- 4138
DB      3905 GGGTTCGCGCACATTTTCCCAAAAAGTCCACCTGTATCGGTGTGAATTCGCCAGC 3846
QY      4139 -----TCAGAAAGACTC 4150
DB      3845 ATGCGTAAGAGAAATAACCGCATCAGAAATTTGAAGGTTAATTAATTCAGAAAGACTC 3786
QY      4151 GTCAAGAAAGCGATTAAGAGCGCATGCGTCCGATTTGGAGCGGCGATTCGGTAAAGCAC 4210
DB      3785 GTCAAGAAAGCGATTAAGAGCGCATGCGTCCGATTTGGAGCGGCGATTCGGTAAAGCAC 3726
QY      4211 GAGGAAGCGGTAGCCCATTTGCGCGCAAGCTCTTACGCAATATCACGGATAGCCACGC 4270
DB      3725 GAGGAAGCGGTAGCCCATTTGCGCGCAAGCTCTTACGCAATATCACGGATAGCCACGC 3666
QY      4271 TATGTCCTGATAGCGGTCCGCCACACCGAGCGGCCACAGTGAATTCAGAAAAGCG 4330
DB      3665 TATGTCCTGATAGCGGTCCGCCACACCGAGCGGCCACAGTGAATTCAGAAAAGCG 3606
QY      4331 GCCATTTTCCACATATATTTGGGCAAGCAGCATGTGCTATGGGTACAGAGATCTCTC 4390
DB      3605 GCCATTTTCCACATATATTTGGGCAAGCAGCATGTGCTATGGGTACAGAGATCTCTC 3546
QY      4391 GCGGTGGGCGATGCGGCTTGAAGCTGTGCGAAACAGTTGCGGCTGGGCGAGGCCCTGATG 4450
DB      3545 GCGGTGGGCGATGCTGCTTGAAGCTGTGCGAAACAGTTGCGGCTGGGCGAGGCCCTGATG 3486
QY      4451 CTCTTGTCCAGATCATCTGATTCGACAAAGACCGGCTTCAATCCAGTACGTGCTGCTC 4510
DB      3485 CTCTTGTCCAGATCATCTGATTCGACAAAGACCGGCTTCAATCCAGTACGTGCTGCTC 3426
QY      4511 GATGCAATGTTTGGCTTGTGTGCTGAATGGGCAAGTATGCCGATCAAGGTTATGACCGG 4570
DB      3425 GATGCAATGTTTGGCTTGTGTGCTGAATGGGCAAGTATGCCGATCAAGGTTATGACCGG 3366
QY      4571 CCGCATTTGATCAGCATGATGATGATCTTCTTCGCGAGGACGAAGGTGAGATGACAGAG 4630
DB      3365 CCGCATTTGATCAGCATGATGATGATCTTCTTCGCGAGGACGAAGGTGAGATGACAGAG 3306
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Qy	4631	ATCTCCGCCCCGACCTTGCCTCCCAATATGACGACCAATGCTCTTCCCGCTTCAATGACAAAGCTC	4690
Db	3305	ATCTCGCCCCGACCTTGCCTCCCAATATGACGACCAATGCTCTTCCCGCTTCAATGACAAAGCTC	3246
Qy	4691	GAGCACAAGCTGGCAAGAAACGCCGCTGGTGGCCAGCAACGATAGCCGGGCGCTCGTC	4750
Db	3245	GAGCACAAGCTGGCAAGAAACGCCGCTGGTGGCCAGCAACGATAGCCGGGCGCTCGTC	3186
Qy	4751	CTGCACTTCATTCAAGGACCGGACAGGTGGTCTTGAACAAAAGAACCGGCGCCCTG	4810
Db	3185	TTGCAGTTTCATTCAAGGACCGGACAGGTGGTCTTGAACAAAAGAACCGGCGCCCTG	3126
Qy	4811	CGCTACACGCCGGGAAACAGCGCGGCAATCAGACAGCGCAATGTCTGTGTGCCAATCAT	4870
Db	3125	CGCTACACGCCGGGAAACAGCGCGGCAATCAGACAGCGCAATGTCTGTGTGCCAATCAT	3066
Qy	4871	GCCGATATAGCTCTTCACCCCAAGCGGCGGAGAACCTGCGTGCATTCATCTGTTCAT	4930
Db	3065	GCCGATATAGCTCTTCACCCCAAGCGGCGGAGAACCTGCGTGCATTCATCTGTTCAT	3006
Qy	4931	CATGCGAAACGATCCTCATCTGTCTTTCATCAGATCTTGATTCCTCCCTGCGCATCAGAT	4990
Db	3005	CATGCGAAACGATCCTCATCTGTCTTTCATCAGATCTTGATTCCTCCCTGCGCATCAGAT	2946
Qy	4991	CTTTGGCGGCAAGAAAGCATCCATTTTACCTTTGAGGGGCTTCCCACTTACAGAGGG	5050
Db	2945	CTTTGGCGGCAAGAAAGCATCCATTTTACCTTTGAGGGGCTTCCCACTTACAGAGGG	2886
Qy	5051	CGCCCAAGCTGGCAATTCGCGTTCGCTTGCATTAATAAACCGCCAGTCTAGCTATCG	5110
Db	2885	CGCCCAAGCTGGCAATTCGCGTTCGCTTGCATTAATAAACCGCCAGTCTAGCTATCG	2826
Qy	5111	CCATGTAAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGGCTTGCGTTTCCCTGTCCA	5170
Db	2825	CCATGTAAAGCCCACTGCAAGCTACCTGCTTTCTCTTTGCGGCTTGCGTTTCCCTGTCCA	2766
Qy	5171	GATAGCCCAAGTAGCTGATCATTCATCCGGGGCAGACACGTTTTCGCGGACGTGGCTTCTA	5230
Db	2765	GATAGCCCAAGTAGCTGATCATTCATCCGGGGCAGACACGTTTTCGCGGACGTGGCTTCTA	2706
Qy	5231	CGTG 5234	
Db	2705	CGTG 2702	
RESULT 12			
US-10-790-455-10/c			
Sequence 10, Application US/10790455			
Publication No. US20040210954A1			
GENERAL INFORMATION:			
APPLICANT: Avigenics, Inc			
TITLE OF INVENTION: Avian Integrase-mediated Transformation			
FILE REFERENCE: A181 1080.1			
CURRENT APPLICATION NUMBER: US/10/790, 455			
CURRENT FILING DATE: 2004-03-01			
NUMBER OF SEQ ID NOS: 12			
SOFTWARE: PatentIn version 3.2			
SEQ ID NO 10			
LENGTH: 6233			
TYPE: DNA			
ORGANISM: Plasmid PCR-XL-TOPO-CMV-pur-attB			
US-10-790-455-10			

Query Match	30.9%	Score 1634.4;	DB 8;	Length 6233;
Best Local Similarity	80.6%;	Pred. No. 0;		
Matches 2082;	Conservative 0;	Mismatches 211;	Indels 291;	Gaps 3;

Q7	Qy
2942	CTTCGCGCTTCTCGGTCACTGACTGACTGCTGCGGTGGTGGCTGGCGGCGAGCGGTAT 3001
6233	CTTCGCGTCTCTCGCTCACTGACTGCTGCGGTGGTGGCTGGCGGCGAGCGGTAT 6174
Qy	3002
	CAGCTCACTCAAAAGCGGTAATACGGTTATCCACGAATCAGGGGATTAACGACGAAAGA 3061

Db	6173	CAGCTCAGCTCAAAAGCGCGTAAACGCGTTATCCACAGAAATCAGGGATTAACGAGAAAGA	611
QY	3062	ACATGTGACAAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCGCGT	3122
Db	6113	ACATGTGACAAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGCGGT	605
QY	3122	TTTTCCATGAGGCTCCGCCCCCTGACGAGCATCAAAAAATGACGCTCCAGTCAAGGT	3188
Db	6053	TTTTCCATGAGGCTCCGCCCCCTGACGAGCATCAAAAAATGACGCTCCAGTCAAGGT	5994
QY	3182	GGCGAAACCCGACAGACTATPAAATPACAGGGGTTTTCCCTGGAAGCTCCCGTGCG	3241
Db	5993	GGCGAAACCCGACAGACTATPAAATPACAGGGGTTTTCCCTGGAAGCTCCCGTGCG	5933
QY	3242	GCTCTCTGTTTCGACCCCTGCGCTTACCGGATACCTGTCGCTCTTCTCCCTTCGGGA	3301
Db	5933	GCTCTCTGTTTCGACCCCTGCGCTTACCGGATACCTGTCGCTCTTCTCCCTTCGGGA	5874
QY	3302	GCGTGCGCTTTCTCATAGCTCAGCGCTGAGGATCTCAGTTCCGCTGTAAGTCTGTCCT	3361
Db	5873	GCGTGCGCTTTCTCATAGCTCAGCGCTGAGGATCTCAGTTCCGCTGTAAGTCTGTCCT	5814
QY	3362	CCAACTGGGCGTGTGACGAAACCCCGGTTACGCGCCGACCGCGCGGCGCTTATCCGGTA	3422
Db	5813	CCAACTGGGCGTGTGACGAAACCCCGGTTACGCGCCGACCGCGCGCTTATCCGGTA	5755
QY	3422	ACTATCGTCTTGAGTCCAAACCCGGAACAGACTTATCCGCACTGCGACAGCCACTG	3481
Db	5755	ACTATCGTCTTGAGTCCAAACCCGGAACAGACTTATCCGCACTGCGACAGCCACTG	5699
QY	3482	GTAACAGATTAGCAGACGAGATATGTAGGCGGTCTACAGAGTTCTTGAAGTGTGGC	3541
Db	5693	GTAACAGATTAGCAGACGAGATATGTAGGCGGTCTACAGAGTTCTTGAAGTGTGGC	5634
QY	3542	CTAATTAAGGCTACATAGAAAGAACAGTATTTGGTATGTGGCGCTCTGTGAAGCCAGTTA	3601
Db	5633	CTAATTAAGGCTACATAGAAAGAACAGTATTTGGTATGTGGCGCTCTGTGAAGCCAGTTA	5574
QY	3602	CCTTCGAAAAAGAGTTGGTAGCTCTTATATCCGGCAACAAACACCGCTGTAGCGGTG	3661
Db	5573	CCTTCGAAAAAGAGTTGGTAGCTCTTATATCCGGCAACAAACACCGCTGTAGCGGTG	5514
QY	3662	GTTTTTTTGTTCGAAAGCAGCAGATTACGCGCAAAAAAAGATCTCCAGAGATCCTT	3721
Db	5513	GTTTTTTTGTTCGAAAGCAGCAGATTACGCGCAAAAAAAGATCTCCAGAGATCCTT	5455
QY	3722	TGATTTTTCTACCGGGGTCTGACGCTCAGTGAACGAAACTCAGCTTAAAGGATTTTGG	3781
Db	5453	TGATTTTTCTACCGGGGTCTGACGCTCAGTGAACGAAACTCAGCTTAAAGGATTTTGG	5394
QY	3782	TCATGAGATTATC-----	3794
Db	5393	TCATGAGATTATCAAAAAAGATCTTACCTAGATCTTTTAAATTAAAAATGAAGTTTAA	5334
QY	3795	-----GTGACCA	3802
Db	5333	GCAAGTGTCAATCCGTCCTCCGCGCACAGAGTCAAGCAGATTGCGCGCGGCTCGCGCA	5274
QY	3803	AAGCGGCATGTGTCCTCCCACTCTCGCAGTTGCGGGCGCATGTGATCGCGGATAGCGCG	3862
Db	5273	GAGGGAATCTCCGCGCCCAACGCGGTCTCGCGCATCTCGGTATAGCGCGCGCGGAGCGGT	5214
QY	3863	TGCTGTGTTCTGTGATGCGGACGGAATTTTGCACTGCGCGGTAGAACTCCGCGAGGTCTGCA	3922
Db	5213	CCCGGAAGTTGTGACACAGCCTCCGACCACTCGGCGTACAGTCTGTCCAGCGCGCGCA	5154
QY	3923	GCC-----	3925
Db	5153	CCCAACCCCAAGGCGAGGTGTTCGCGGCAACACTGTGTCTTGACCGCGCTGATGTAACA	5094
QY	3926	---TGAAGCAGACTGAACCAACTGCGCAGAGGAGTCAAGCCCGGGGTGGCGAAGAACT	3982
Db	5093	GAGTCAAGTGTCTCCCGGACCAACCGCGGAAAGTGTCTTCAAGAGTCCCGGAGAAAC	5034

QY 3302 GCGTGGCGCTTTCTCATAGCTACGCTGATGATCTCAGTTGCGTAGTGCTGCT 3361
 DB 5873 GGGTGGCGCTTTCTCATAGCTACGCTGATGATCTCAGTTGCGTAGTGCTGCT 5814
 QY 3362 CCAAGTGGGCTGTGTGCAAGAACCCCGGTTACGCCGACCGCTGCGCTTATCCGGTA 3421
 DB 5813 CCAAGTGGGCTGTGTGCAAGAACCCCGGTTACGCCGACCGCTGCGCTTATCCGGTA 5754
 QY 3422 ACTATGCTTGTAGTCAACCCGGTAAACAAGACTTATCGCACTGCGAGACGACACTG 3481
 DB 5753 ACTATGCTTGTAGTCAACCCGGTAAACAAGACTTATCGCACTGCGAGACGACACTG 5694
 QY 3482 GTAACGAGATTAGCAGAGGAGATATGAGCGGTGCTACAGAGTTCTTGAAGTGTGC 3541
 DB 5693 GTAACGAGATTAGCAGAGGAGATATGAGCGGTGCTACAGAGTTCTTGAAGTGTGC 5634
 QY 3542 CTAACTACGGCTACACTAGAAAGACATATTTGTATCTGCGCTCTGTAAGCCAGTTA 3601
 DB 5633 CTAACTACGGCTACACTAGAAAGACATATTTGTATCTGCGCTCTGTAAGCCAGTTA 5574
 QY 3602 CTTTGGAAAAAGATGTGTAGCTCTGTATCCGGCAACAACCCGCTGTAGCGGTG 3661
 DB 5573 CTTTGGAAAAAGATGTGTAGCTCTGTATCCGGCAACAACCCGCTGTAGCGGTG 5514
 QY 3662 GTTTTTTGTGTGCAAGCAGAGATTACCGCAAGAAAAAGATCTCAAGAATCTT 3721
 DB 5513 GTTTTTTGTGTGCAAGCAGAGATTACCGCAAGAAAAAGATCTCAAGAATCTT 5454
 QY 3722 TGATCTTTTCTAGGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGATTTTG 3781
 DB 5453 TGATCTTTTCTAGGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGATTTTG 5394
 QY 3782 TCATGAGATTATC----- 3794
 DB 5393 TCATGAGATTATCAAAAAAGATCTTCACTAGATCTTTTAAATTAAGATTTTA 5334
 QY 3795 -----GTGACCA 3802
 DB 5333 GCACGTGTCAGTCTGCTCTCGGCGCAAGAGTGAACGACGATGCGCGCGGCTGCGCA 5274
 QY 3803 AAGCGGCATGTGCTCTCCCACTCTCTGACGTTGCGGGGATGATGCGCGGATAGCCG 3862
 DB 5273 GGGCGAATCTCCGCGCCCGACGCTGCTGCGCGATCTCGGTCAATGCGCGCGGCGGCGT 5214
 QY 3863 TGCTGTGTTTCCGTGATGCGGACGAGATTGTCATGCGCGGTAAACCTCCCGAGGTGTCA 3922
 DB 5213 CCGGAGATTGTGACACGACCTCGAACCACTCGGCTGACAGCTGTCAGGCGCGCA 5154
 QY 3923 GGC----- 3925
 DB 5153 CCGACACCCAGGCGAGGTGTTGTCCGACCACTGCTGACCCGCGCTGATGAACA 5094
 QY 3926 ---TCAGGACGAGTGAACCACTGCGAGGGATGACCCGCGGTGGCGAAGACT 3982
 DB 5093 GGGTCACTGCTCTCCGACCAACCGCGAAGTCTCTTCCAGAAATGCCGGAGAAC 5034
 QY 3983 CCGAGATGAGATCCCGCGCTGAGAGATCTCAGCCGCGCTCCGGAAGATTCGCA 4042
 DB 5033 CGAGCGGTGCTGACAGACTGACCGCTCCGCGACGCTCGCGCGGTGAGCAACCGGAA 4974
 QY 4043 AGCCCACTTTTCAATAGAGCGCGGATGAACTCGTGAATGGCAGGTTGGCG 4102
 DB 4973 CGGCACTGGTCACTGGGCACTGTGTGCGCTCTCAGCGTCTATTTATGAAGCATTTATC 4914
 QY 4103 TCGCTTGTGCTATTTTGAACCCCGAGATCCG----- 4137
 DB 4913 AGGGTATTTGTCTATGAGCGGATACATATTTGAATGATAAATAAACAATAG 4854
 QY 4138 ----- 4137
 DB 4853 GGGTTCGCGCACATTTCCCGAAAAATGCACTGTATGCGGTGTGAATAACGCAAG 4794
 QY 4138 -----CTCAGAGAACTC 4150

DB 4793 ATCGTAAAGAAAAATACCGCATCAGAAATTTGTAAGCTTAAATTCAGAAATCTC 4734
 QY 4151 GTCAAGAAAGCGATAGAAAGCGATGCGCTGCAATCGGAGCGCGATACCGTAAAGCAC 4210
 DB 4733 GTCAAGAAAGCGATAGAAAGCGATGCGCTGCAATCGGAGCGCGATACCGTAAAGCAC 4674
 QY 4211 GAGAAAGCGTCAAGCCATTCGCGCCAAAGCTCTTACGATATATCACGGTATGCCAAGC 4270
 DB 4673 GAGAAAGCGTCAAGCCATTCGCGCCAAAGCTCTTACGATATATCACGGTATGCCAAGC 4614
 QY 4271 TATGCTGATAGCGGTCCGCCACACCCAGCGCGCACAGTGTGATGAAATCCAGAAAGCG 4330
 DB 4613 TATGCTGATAGCGGTCCGCCACACCCAGCGCGCACAGTGTGATGAAATCCAGAAAGCG 4554
 QY 4331 GCCATTTTCAACATGATATTTGCGAAGCAGGATCGCATAGGTCAAGACGAGATCTTC 4390
 DB 4553 GCCATTTTCAACATGATATTTGCGAAGCAGGATCGCATAGGTCAAGACGAGATCTTC 4494
 QY 4391 GCCGTGGGCAATGCGCGCTTGAAGCTGCGCAAGATTGCGCTGCGCGAGCCCTGATG 4450
 DB 4493 GCCGTGGGCAATGCGCGCTTGAAGCTGCGCAAGATTGCGCTGCGCGAGCCCTGATG 4434
 QY 4451 CTCTTGTCCAGATCATCTGATCGACAAAGACCGGCTTCAATCCGAGTACGTCGCTC 4510
 DB 4433 CTCTTGTCCAGATCATCTGATCGACAAAGACCGGCTTCAATCCGAGTACGTCGCTC 4374
 QY 4511 GATGCGATGTTTGTGTTGTGTGATGAGTGGCAGGTAGCCGATCAAGCTATGACGCG 4570
 DB 4373 GATGCGATGTTTGTGTTGTGTGATGAGTGGCAGGTAGCCGATCAAGCTATGACGCG 4314
 QY 4571 CCGCATTTGATCAGCATGATGATGATCTTTCTCGCAGAGACAAAGTGAATGACAGAG 4630
 DB 4313 CCGCATTTGATCAGCATGATGATGATCTTTCTCGCAGAGACAAAGTGAATGACAGAG 4254
 QY 4631 ATCTGCCCCGCACTTGCGCCCAATAGACGACGATCCCTTCCGCTTCAAGAACAGTTC 4690
 DB 4253 ATCTGCCCCGCACTTGCGCCCAATAGACGACGATCCCTTCCGCTTCAAGAACAGTTC 4194
 QY 4691 GAGCAGAGCTGCGCAAGAAAGCGCGCTGTGCGCAGCAGATAGCGCGCTGCTGTC 4750
 DB 4193 GAGCAGAGCTGCGCAAGAAAGCGCGCTGTGCGCAGCAGATAGCGCGCTGCTGTC 4134
 QY 4751 CTGAGATTCAATCAGGGCACTGCAAGGTGCTTGAACAAAAGAACCGGCGCCCTG 4810
 DB 4133 TTGAGATTCAATCAGGGCACTGCAAGGTGCTTGAACAAAAGAACCGGCGCCCTG 4074
 QY 4811 CGTGAAGCGGAAACAAGGCGCATCAGAGCAGCGATGTCGTTGTGTCGCGCATTA 4870
 DB 4073 CGTGAAGCGGAAACAAGGCGCATCAGAGCAGCGATGTCGTTGTGTCGCGCATTA 4014
 QY 4871 GCCGAATAGCTTCAACCAAGCGCGGAGAACTGCGTGAATCAATCTTGTTCAT 4930
 DB 4013 GCCGAATAGCTTCAACCAAGCGCGGAGAACTGCGTGAATCAATCTTGTTCAT 3954
 QY 4931 CATGCGAAAGATCTTATCTGCTCTTGTATCAGATCTTGAATCCCTGGCCATCAGAT 4990
 DB 3953 CATGCGAAAGATCTTATCTGCTCTTGTATCAGATCTTGAATCCCTGGCCATCAGAT 3894
 QY 4991 CTTTGGCGGCAAGAAAGCAATCCAGTTTACCTTTCAGAGGCTTCCCACTTACAGAGGG 5050
 DB 3893 CTTTGGCGGCAAGAAAGCAATCCAGTTTACCTTTCAGAGGCTTCCCACTTACAGAGGG 3834
 QY 5051 CGCCCAAGCTGCAATTCGAGTTGCTGCTGTGCTCATAAACCGCCAGTCTAGCTATCG 5110
 DB 3833 CGCCCAAGCTGCAATTCGAGTTGCTGCTGTGCTCATAAACCGCCAGTCTAGCTATCG 3774
 QY 5111 CCAATGTAAGCCCACTGCAAGCTGCTTCTTCTTTCGCTGCGTTTTCCTTGTCA 5170
 DB 3773 CCAATGTAAGCCCACTGCAAGCTGCTTCTTCTTTCGCTGCGTTTTCCTTGTCA 3714
 QY 5171 GATAGCCCAATGATGATTCATCCGCGGTGAGACCGTTTCGCGGATCGGCTTTCTA 5230

Db 5333 GCACGTGTCAAGTCTCGTCTCTCGGCAAGAAAGTGCAGAGTTGGCCGGGCTGGGCA 5274
Qy 3803 AAGGGCCATGTGTCCTTCCCACTCTGCAAGTTGGGGGCAATGAGTGGCGGATAGCCGC 3862
Db 5273 GGGGAACTCCCGCCCCCAAGGCTGCTGCGGATCTCGGTCAATGCGCGCCGGAAGCGT 5214
Qy 3863 TGTGTGTTCTGTGATGCGAGGATTTGCACTGCGGATGAACTCCGCGAGTCTGCA 3922
Db 5213 CCGGAAAGTTGTGTGACACGACCTCCGACCACTGGGGTACAGCTTCCTCAGGCCGCGCA 5154
Qy 3923 GCC----- 3925
Db 5153 CCCACACCCAGGCGAGGTGTTGTCCGGCACCACTGGTCTTGAGCCGCGTGAACA 5094
Qy 3926 ---TCAGGCAAGCACTGAACCACTCGGAGGGATGAGGCCGGGGTGGCGGAAGACT 3982
Db 5093 GGGTACGTCGTCCCGACACACCGGAGTGTCTTCCACAAAGTCCCGGAGAAC 5034
Qy 3983 CCAGCATGAGATCCCGCGCTGAGAGATCATCCAGCGGCGTCCGGAAAAAGATTCCGA 4042
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Db 4913 AGGGTTATTGTCTCATAGCGGAATACATTTGAATGATTAGAAAAATMAACAATAG 4854
Qy 4138 ----- 4137
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Qy 5231 CGTG 5234
Db 3653 CGTG 3650

Search completed: May 14, 2006, 08:15:56
Job time : 2599 secs

November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbn** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions

.rapbn (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.8
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OM nucleic - nucleic search, using bw model

Run on: May 14, 2006, 07:33:51 ; Search time 1435 seconds
(without alignments)
15015.205 Million cell updates/sec

Title: US-09-921-143-36

Perfect score: 5283
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Scoring table: IDENTITY NUC
Gap 10'-0, Gapext 1.0

Searched: 9312410 seqs, 2039259788 residues

Total number of hits satisfying chosen parameters: 10624020

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5283	100.0	5283	18	US-11-249-422-36
2	1692.4	32.0	17	US-11-231-725-1	Sequence 36, Appli
3	1634.4	30.9	13	US-10-517-698-1	Sequence 1, Appli
4	1634.4	30.9	17	US-11-193-750-10	Sequence 10, Appli
5	1603.8	30.4	11	US-10-764-818A-11	Sequence 11, Appli
6	1603.8	30.4	11	US-10-764-818A-12	Sequence 12, Appli
7	1603.8	30.4	11	US-10-764-818A-13	Sequence 13, Appli
8	1603.8	30.4	11	US-10-764-818A-14	Sequence 14, Appli
9	1603.8	30.4	11	US-10-764-818A-15	Sequence 15, Appli
10	1603.8	30.4	11	US-11-186-282-22	Sequence 22, Appli
11	1603.8	30.4	17	US-11-186-282-22	Sequence 29, Appli
12	1603.4	30.4	11	US-10-764-818A-26	Sequence 26, Appli
13	1572.6	29.8	18	US-11-194-143-27	Sequence 27, Appli
14	1570	29.7	17	US-11-005-216-4	Sequence 4, Appli

C 15	1569.8	29.7	4151	17	US-11-213-368-15	Sequence 15, Appli
C 16	1569.8	29.7	4181	17	US-11-170-123-1	Sequence 1, Appli
C 17	1569.8	29.7	4181	17	US-11-170-123-2	Sequence 2, Appli
C 18	1569.8	29.7	4692	17	US-11-082-154A-29	Sequence 29, Appli
C 19	1569.8	29.7	4862	17	US-11-082-154A-87	Sequence 87, Appli
C 20	1569.8	29.7	4894	17	US-11-181-148-2	Sequence 2, Appli
C 21	1569.8	29.7	7487	17	US-11-181-148-4	Sequence 4, Appli
C 22	1568.2	29.7	3913	10	US-10-981-267-27	Sequence 27, Appli
C 23	1557	29.5	5181	17	US-11-094-484-3	Sequence 3, Appli
C 24	1552.6	29.4	5031	18	US-11-149-420-64	Sequence 64, Appli
C 25	1552.6	29.4	6914	18	US-11-149-420-61	Sequence 61, Appli
C 26	1552.6	29.4	7341	18	US-11-149-420-66	Sequence 66, Appli
C 27	1546.6	29.3	4855	11	US-10-764-818A-27	Sequence 27, Appli
C 28	1490.4	28.2	3974	17	US-11-205-031-10	Sequence 10, Appli
C 29	1490.4	28.2	3974	17	US-11-233-119-16	Sequence 16, Appli
C 30	1490.4	28.2	3974	18	US-11-048-774-14	Sequence 14, Appli
C 31	1490.4	28.2	3974	18	US-11-249-422-16	Sequence 16, Appli
C 32	1487.2	28.2	8687	14	US-11-297-317-15	Sequence 15, Appli
C 33	1487.2	28.2	8687	14	US-11-297-317-16	Sequence 16, Appli
C 34	1487.2	28.2	9362	14	US-11-297-317-18	Sequence 18, Appli
C 35	1487.2	28.2	9400	14	US-11-297-317-17	Sequence 17, Appli
C 36	1487.2	28.2	12445	11	US-10-948-344-2	Sequence 2, Appli
C 37	1462	27.7	8136	17	US-11-082-154A-31	Sequence 31, Appli
C 38	1462	27.7	17384	17	US-11-082-154A-118	Sequence 118, App
C 39	1389.2	26.3	2403	11	US-10-523-682-1	Sequence 1, Appli
C 40	1388.6	26.3	2722	17	US-11-186-282-23	Sequence 23, Appli
C 41	1388.6	26.3	2725	17	US-11-186-282-24	Sequence 24, Appli
C 42	1387	26.3	2700	17	US-11-186-282-33	Sequence 33, Appli
C 43	1387	26.3	2716	11	US-10-764-818A-19	Sequence 19, Appli
C 44	1387	26.3	2716	11	US-10-764-818A-20	Sequence 20, Appli
C 45	1387	26.3	2716	17	US-11-186-282-27	Sequence 27, Appli

ALIGNMENTS

RESULT 1	US-11-249-422-36
Sequence 36, Application US/11249422	
Publication No. US20060057117A1	
GENERAL INFORMATION:	
APPLICANT: Coleman, Timothy	
TITLE OF INVENTION: Vascular Endothelial Growth Factor-2	
FILE REFERENCE: P112P6C1	
CURRENT APPLICATION NUMBER: US/11/249,422	
CURRENT FILING DATE: 2005-10-14	
PRIOR APPLICATION NUMBER: 09/921,143	
PRIOR FILING DATE: 2001-08-03	
PRIOR APPLICATION NUMBER: 60/223,276	
PRIOR FILING DATE: 2000-08-04	
NUMBER OF SEQ ID NOS: 36	
SOFTWARE: PatentIn version 3.0	
SEQ ID NO 36	
LENGTH: 5283	
TYPE: DNA	
ORGANISM: homo sapiens	
US-11-249-422-36	
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Best local similarity	100.0%; Pred. No. 0;
Matches 5283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB 61	TACCATGATGATGCGGTTTGGAGAGTACATCATATGCGGTTAGCTACGACG 120
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DB 121	GGAATTTCCAGATCTCACCCACATGACATGAGGAGTTTGGACCAATCA 180

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QY	301	CATGCCGATTTGGTGGAGGTAAAGTGTATGATCGTGTATGATCGTGCCTTTGTAGAG	360
Db	301	CATGCCGATTTGGTGGAGGTAAAGTGTATGATCGTGTATGATCGTGCCTTTGTAGAG	360
QY	361	GCAACAGACGGGCTCTTAACAACGGAATTGACGAACCACTGAATTCCGCATTGCAGATATT	420
Db	361	GCAACAGACGGGCTCTTAACAACGGAATTGACGAACCACTGAATTCCGCATTGCAGATATT	420
QY	421	GTATTTAATGTCGCCAGCTCCGATTAACAATAAGCCATTGACCATTCACCACTTGGTGTG	480
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QY	481	CACCTGGGTTGGAGTCGATTCATCATGCACTGCGAGGCTTCTCTGTGGCGTGTCT	540
Db	481	CACCTGGGTTGGAGTCGATTCATCATGCACTGCGAGGCTTCTCTGTGGCGTGTCT	540
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QY	781	AACAGAGAAACGGCCCACTCAACCTCAAGGACAGAAAGACATATAAATTTGCTGCACGA	840
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QY	1981	GTGCTTAAGTGTGGAGGGTCTCAGGCTTAACCAATGGAGGAGCACATTTCTGTGGGACGT	2040
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2701 GCTGTCTAGAGTATCATGTGCTATGCTGTTTCTGTGTGAATTTGTTATCCGCTCA 2760
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Qy 2761 ATTCCACAACAATACGAGCGGAGAACTAAAGTAAAGCTGGGGGCTTAATGAGTG 2820
2761 ATTCCACAACAATACGAGCGGAGAACTAAAGTAAAGCTGGGGGCTTAATGAGTG 2820
Db 2761 ATTCCACAACAATACGAGCGGAGAACTAAAGTAAAGCTGGGGGCTTAATGAGTG 2820
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Qy 2821 AGCTACTACATTAATTTGCGTGGCTCACTGCGCGCTTTCAGTGTGGAAACCTGTG 2880
2821 AGCTACTACATTAATTTGCGTGGCTCACTGCGCGCTTTCAGTGTGGAAACCTGTG 2880
Db 2821 AGCTACTACATTAATTTGCGTGGCTCACTGCGCGCTTTCAGTGTGGAAACCTGTG 2880
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Qy 2881 TGGCAGCTGCATTATGATATGCGCAACGCGGGGAGAGGCGGTTTGCATTGGGCGC 2940
2881 TGGCAGCTGCATTATGATATGCGCAACGCGGGGAGAGGCGGTTTGCATTGGGCGC 2940
Db 2881 TGGCAGCTGCATTATGATATGCGCAACGCGGGGAGAGGCGGTTTGCATTGGGCGC 2940
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Qy 2941 TCTTCGCGCTTCCTGCTCACTGACTGCTGGCTGGCTGGCTGGCTGGCGGAGCGGTA 3000
2941 TCTTCGCGCTTCCTGCTCACTGACTGCTGGCTGGCTGGCTGGCTGGCGGAGCGGTA 3000
Db 2941 TCTTCGCGCTTCCTGCTCACTGACTGCTGGCTGGCTGGCTGGCTGGCGGAGCGGTA 3000
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Qy 3001 TCAAGCTCACTCAAAAGCGGTATACGGTATTCACAGATCAGGGGATTAACGACGAAAG 3060
3001 TCAAGCTCACTCAAAAGCGGTATACGGTATTCACAGATCAGGGGATTAACGACGAAAG 3060
Db 3001 TCAAGCTCACTCAAAAGCGGTATACGGTATTCACAGATCAGGGGATTAACGACGAAAG 3060
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Qy 3061 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAACGTTAAAAAGCCGCGCTGTGCG 3120
3061 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAACGTTAAAAAGCCGCGCTGTGCG 3120
Db 3061 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAACGTTAAAAAGCCGCGCTGTGCG 3120
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Qy 3121 TTTTTCATAGGCTCGCGCCCCCTGACGAGCATACAAAAATGACGCTCAAGTCAAGG 3180
3121 TTTTTCATAGGCTCGCGCCCCCTGACGAGCATACAAAAATGACGCTCAAGTCAAGG 3180
Db 3121 TTTTTCATAGGCTCGCGCCCCCTGACGAGCATACAAAAATGACGCTCAAGTCAAGG 3180
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Qy 3181 TGGCGAAACCCGACAGAGACTATAAGATACAGAGCGTTTCCCTCGAAGGCTCCCTG 3240
3181 TGGCGAAACCCGACAGAGACTATAAGATACAGAGCGTTTCCCTCGAAGGCTCCCTG 3240
Db 3181 TGGCGAAACCCGACAGAGACTATAAGATACAGAGCGTTTCCCTCGAAGGCTCCCTG 3240
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Qy 3241 CGCTCTCTGTTCGACCTGCGCTTACCGGATACCTGTCCGCTTTCCTCCCTGCGGA 3300
3241 CGCTCTCTGTTCGACCTGCGCTTACCGGATACCTGTCCGCTTTCCTCCCTGCGGA 3300
Db 3241 CGCTCTCTGTTCGACCTGCGCTTACCGGATACCTGTCCGCTTTCCTCCCTGCGGA 3300
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Qy 3301 AGGATGGCGCTTCTCATAGTCAAGCTGTAGATATTCAGATTGGGTAGTGTTCGCG 3360
3301 AGGATGGCGCTTCTCATAGTCAAGCTGTAGATATTCAGATTGGGTAGTGTTCGCG 3360
Db 3301 AGGATGGCGCTTCTCATAGTCAAGCTGTAGATATTCAGATTGGGTAGTGTTCGCG 3360
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Qy 3361 TCCAGAGCTGGAGCTGTGTGCAAGAACCCCGCTTCAAGCCGAGCTGCGCTTATCCGGT 3420
3361 TCCAGAGCTGGAGCTGTGTGCAAGAACCCCGCTTCAAGCCGAGCTGCGCTTATCCGGT 3420
Db 3361 TCCAGAGCTGGAGCTGTGTGCAAGAACCCCGCTTCAAGCCGAGCTGCGCTTATCCGGT 3420
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Qy 3421 AACCTATGTCTTGAATCAACCCGGTAAAGACGACTTATGCGCACTGGACAGCGCACT 3480
3421 AACCTATGTCTTGAATCAACCCGGTAAAGACGACTTATGCGCACTGGACAGCGCACT 3480
Db 3421 AACCTATGTCTTGAATCAACCCGGTAAAGACGACTTATGCGCACTGGACAGCGCACT 3480

|||||
Db 3421 AACCTATGTCTTGAATCAACCCGGTAAAGACGACTTATGCGCACTGGACAGCGCACT 3480
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Qy 3481 GGTAAACGATTTACAGAGCGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGTG 3540
3481 GGTAAACGATTTACAGAGCGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGTG 3540
Db 3481 GGTAAACGATTTACAGAGCGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGTG 3540
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Qy 3541 CCTAACCTACCGCTACACTAGAGAAAGATATTTGTATCTGCGCTGTGTAACCACTT 3600
3541 CCTAACCTACCGCTACACTAGAGAAAGATATTTGTATCTGCGCTGTGTAACCACTT 3600
Db 3541 CCTAACCTACCGCTACACTAGAGAAAGATATTTGTATCTGCGCTGTGTAACCACTT 3600
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Qy 3601 ACCTTCGAAAAAAGATTGGTAGCTTTGATTCGCGCAAAACCAACCGCTGTAGCGGT 3660
3601 ACCTTCGAAAAAAGATTGGTAGCTTTGATTCGCGCAAAACCAACCGCTGTAGCGGT 3660
Db 3601 ACCTTCGAAAAAAGATTGGTAGCTTTGATTCGCGCAAAACCAACCGCTGTAGCGGT 3660
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Qy 3661 GGTTTTTTTGTTTGAAGAGCAAGATTAAACGGCAAAAAAAGATCTCAAGAAAGATCT 3720
3661 GGTTTTTTTGTTTGAAGAGCAAGATTAAACGGCAAAAAAAGATCTCAAGAAAGATCT 3720
Db 3661 GGTTTTTTTGTTTGAAGAGCAAGATTAAACGGCAAAAAAAGATCTCAAGAAAGATCT 3720
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Qy 3721 TTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCAGCTTAAGGATTTTG 3780
3721 TTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCAGCTTAAGGATTTTG 3780
Db 3721 TTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCAGCTTAAGGATTTTG 3780
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Qy 3781 GTCATGAGATTATGCTGACCAAAAGCGGCATCGTGCCTCCCACTCTGTGAGTTGCGGG 3840
3781 GTCATGAGATTATGCTGACCAAAAGCGGCATCGTGCCTCCCACTCTGTGAGTTGCGGG 3840
Db 3781 GTCATGAGATTATGCTGACCAAAAGCGGCATCGTGCCTCCCACTCTGTGAGTTGCGGG 3840
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Qy 3841 GCATGAGTGGCGGATGACCGCTGCTGTTTCTGATATGCCAGAGATTTGCATGCGCG 3900
3841 GCATGAGTGGCGGATGACCGCTGCTGTTTCTGATATGCCAGAGATTTGCATGCGCG 3900
Db 3841 GCATGAGTGGCGGATGACCGCTGCTGTTTCTGATATGCCAGAGATTTGCATGCGCG 3900
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Qy 3901 TAGAACTCCGCGAGTGTGCTCAGCGCTCAGGACAGAGCTGAAACCACTCGGAGGGATTCG 3960
3901 TAGAACTCCGCGAGTGTGCTCAGCGCTCAGGACAGAGCTGAAACCACTCGGAGGGATTCG 3960
Db 3901 TAGAACTCCGCGAGTGTGCTCAGCGCTCAGGACAGAGCTGAAACCACTCGGAGGGATTCG 3960
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Qy 3961 AGCCCGGGTGGCGAAAGAACTCCAGCATGAGATCCCGGCTGAGAGATCATCAACCG 4020
3961 AGCCCGGGTGGCGAAAGAACTCCAGCATGAGATCCCGGCTGAGAGATCATCAACCG 4020
Db 3961 AGCCCGGGTGGCGAAAGAACTCCAGCATGAGATCCCGGCTGAGAGATCATCAACCG 4020
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Qy 4021 GCGTCCCGGAAACGATTCGGAAGCCCACTTTCATAGAAAGCGGGGTGGAATCCAAA 4080
4021 GCGTCCCGGAAACGATTCGGAAGCCCACTTTCATAGAAAGCGGGGTGGAATCCAAA 4080
Db 4021 GCGTCCCGGAAACGATTCGGAAGCCCACTTTCATAGAAAGCGGGGTGGAATCCAAA 4080
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Qy 4081 TCTCGTATGGCAGTGTGGCGCTGCTGCTGCGTCAATTCGAAACCCAGAGTCCCGCTC 4140
4081 TCTCGTATGGCAGTGTGGCGCTGCTGCTGCGTCAATTCGAAACCCAGAGTCCCGCTC 4140
Db 4081 TCTCGTATGGCAGTGTGGCGCTGCTGCTGCGTCAATTCGAAACCCAGAGTCCCGCTC 4140
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Qy 4141 AGAAGAACTGCTCAAGAAAGCGATAGAAAGCGATGCGCTGCAATCGGAGCGGCAATAC 4200
4141 AGAAGAACTGCTCAAGAAAGCGATAGAAAGCGATGCGCTGCAATCGGAGCGGCAATAC 4200
Db 4141 AGAAGAACTGCTCAAGAAAGCGATAGAAAGCGATGCGCTGCAATCGGAGCGGCAATAC 4200
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Qy 4201 CGTAAAGCAAGAAAGCGGTCAAGCCATTCGCGCGCCAACTCTTCAGCAATATCAAGG 4260
4201 CGTAAAGCAAGAAAGCGGTCAAGCCATTCGCGCGCCAACTCTTCAGCAATATCAAGG 4260
Db 4201 CGTAAAGCAAGAAAGCGGTCAAGCCATTCGCGCGCCAACTCTTCAGCAATATCAAGG 4260
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Qy 4261 TAGCAACGCTATGCTCTGATAGCGGTGCGCAACCCAGCGGCAAGATGATGATC 4320
4261 TAGCAACGCTATGCTCTGATAGCGGTGCGCAACCCAGCGGCAAGATGATGATC 4320
Db 4261 TAGCAACGCTATGCTCTGATAGCGGTGCGCAACCCAGCGGCAAGATGATGATC 4320
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Qy 4321 CAGAAAAAGCGCAATTTTCCACCATGATATTCGGAAGAGAGCATGCGCATGGGTACGA 4380
4321 CAGAAAAAGCGCAATTTTCCACCATGATATTCGGAAGAGAGCATGCGCATGGGTACGA 4380
Db 4321 CAGAAAAAGCGCAATTTTCCACCATGATATTCGGAAGAGAGCATGCGCATGGGTACGA 4380
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Qy 4381 CGAGATCTTCGCGGTGGGATGCGCGCTTGAAGCTGTGGGAAACAGTTCCGCTGGCGGA 4440
4381 CGAGATCTTCGCGGTGGGATGCGCGCTTGAAGCTGTGGGAAACAGTTCCGCTGGCGGA 4440
Db 4381 CGAGATCTTCGCGGTGGGATGCGCGCTTGAAGCTGTGGGAAACAGTTCCGCTGGCGGA 4440
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Qy 4441 GCCCTGATGCTCTTGTCTCAGATCATCTGATCGAACAGACGGGCTTCATCCGAGTAC 4500
4441 GCCCTGATGCTCTTGTCTCAGATCATCTGATCGAACAGACGGGCTTCATCCGAGTAC 4500
Db 4441 GCCCTGATGCTCTTGTCTCAGATCATCTGATCGAACAGACGGGCTTCATCCGAGTAC 4500
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Qy 4501 GTGCTGCTCGATGAGATGTTTGTGTTGATGATGGAATGGGAGGTAGCCGATCAAGCG 4560
4501 GTGCTGCTCGATGAGATGTTTGTGTTGATGATGGAATGGGAGGTAGCCGATCAAGCG 4560
Db 4501 GTGCTGCTCGATGAGATGTTTGTGTTGATGATGGAATGGGAGGTAGCCGATCAAGCG 4560

QY 4561 TATGACGCGCCGATTCATGACCATGATGATACTTCTGCGCAGAGCAAGGTAG 4620
DB 4561 TATGACGCGCCGATTCATGACCATGATGATACTTCTGCGCAGAGCAAGGTAG 4620
QY 4621 ATGACAGAGATCTGCGCCGCACTTGGCCCAATGACAGCCGATCCCTTCCGCTTCA 4680
DB 4621 ATGACAGAGATCTGCGCCGCACTTGGCCCAATGACAGCCGATCCCTTCCGCTTCA 4680
QY 4681 TGACCAAGTGCAGACAGCTGCGCAAGGAAGCCCGCTGCGCAGCAAGATGACCGCG 4740
DB 4681 TGACCAAGTGCAGACAGCTGCGCAAGGAAGCCCGCTGCGCAGCAAGATGACCGCG 4740
QY 4741 CTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4800
DB 4741 CTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4800
QY 4801 GCGCGCCCTGCGCTGACAGCCGGAACAGCGCGCATGACAGCCGATGCTGCTGCTG 4860
DB 4801 GCGCGCCCTGCGCTGACAGCCGGAACAGCGCGCATGACAGCCGATGCTGCTGCTG 4860
QY 4861 CCCAGTCATAGCCGAATAGCTCTCCACCCAGCGCGCAAGCCGCTGCTGCTGCTGCT 4920
DB 4861 CCCAGTCATAGCCGAATAGCTCTCCACCCAGCGCGCAAGCCGCTGCTGCTGCTGCT 4920
QY 4921 CTTGTTCAATCATGCGAAACGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4980
DB 4921 CTTGTTCAATCATGCGAAACGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4980
QY 4981 GGCATCATGATCTGCTGCGCGCAAGGAAGCCATCCAGTTTACTTTCAGGGCTTCCAACT 5040
DB 4981 GGCATCATGATCTGCTGCGCGCAAGGAAGCCATCCAGTTTACTTTCAGGGCTTCCAACT 5040
QY 5041 TACCAAGAGGCGCGCCAGCTGCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5100
DB 5041 TACCAAGAGGCGCGCCAGCTGCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5100
QY 5101 CTAGCTATGCGCATGTAAGCCCACTGCAAGCTACTGCTTCTGCTGCTGCTGCTGCT 5160
DB 5101 CTAGCTATGCGCATGTAAGCCCACTGCAAGCTACTGCTTCTGCTGCTGCTGCTGCT 5160
QY 5161 CCTTGTCCAGATGAGCCCACTGATGATCATTCGCGGGTCAAGCCGTTTCTGCGGAC 5220
DB 5161 CCTTGTCCAGATGAGCCCACTGATGATCATTCGCGGGTCAAGCCGTTTCTGCGGAC 5220
QY 5221 TGCTTTCTACGCTTCCGCTTCTTTCAGAGCCCTTTCGCGCGCTGCTGCTGCTGCTG 5280
DB 5221 TGCTTTCTACGCTTCCGCTTCTTTCAGAGCCCTTTCGCGCGCTGCTGCTGCTGCTG 5280
QY 5281 GTG 5283
DB 5281 GTG 5283

RESULT 2
US-11-231-725-1/c
; Sequence 1, Application US/11231725
; Publication No. US20060024821A1
; GENERAL INFORMATION:
; APPLICANT: Palmet, Kenneth E.
; APPLICANT: Pogue, Gary P.
; TITLE OF INVENTION: ROLLING CIRCLE REPLICATION EXPRESSION VECTORS
; FILE REFERENCE: 60-017901US
; CURRENT APPLICATION NUMBER: US/11/231, 725
; PRIOR FILING DATE: 2005-09-20
; PRIOR APPLICATION NUMBER: US/10/286,186
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 5225
; TYPE: DNA
; ORGANISM: Porcine Circovirus

US-11-231-725-1
Query Match 32.0%; Score 1692.4; DB 17; Length 5225;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 2087; Conservative 0; Mismatches 206; Indels 231; Gaps 4;
QY 2942 CTTCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3001
DB 5225 CTTCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3001
QY 3002 CAGCTCACTCAAGGCGGTATACGTTATCCACAGATACAGGAGTATACGAGAAAGA 3061
DB 5165 CAGCTCACTCAAGGCGGTATACGTTATCCACAGATACAGGAGTATACGAGAAAGA 3061
QY 3062 ACATGAGCAAAAGGCGCAAGAAAGCCAGGAACCGTAAAGAGCGCGCTGCGCTG 3121
DB 5105 ACATGAGCAAAAGGCGCAAGAAAGCCAGGAACCGTAAAGAGCGCGCTGCGCTG 3121
QY 3122 TTTTCCATAGGCTCCGCGCCCTGACAGCATCAGAAATCGACGCTCAAGTCAAGGT 3181
DB 5045 TTTTCCATAGGCTCCGCGCCCTGACAGCATCAGAAATCGACGCTCAAGTCAAGGT 3181
QY 3182 GCGGAAACCCGACAGAGCTATTAAGATACAGGCGTTTCCCTGGAAGCTCCCTGCTG 3241
DB 4985 GCGGAAACCCGACAGAGCTATTAAGATACAGGCGTTTCCCTGGAAGCTCCCTGCTG 3241
QY 3242 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3301
DB 4925 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3301
QY 3302 GCGTGGCGCTTCTCATGACTCAAGCTGATGATGATGATGATGATGATGATGATGAT 3361
DB 4865 GCGTGGCGCTTCTCATGACTCAAGCTGATGATGATGATGATGATGATGATGATGAT 3361
QY 3362 CCAAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3421
DB 4805 CCAAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3421
QY 3422 ACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3481
DB 4745 ACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3481
QY 3482 GTAACAGATTAAGCAGAGCGAGGATGATGAGCGGTGCTACAGATTCCTTGAAGTGTG 3541
DB 4685 GTAACAGATTAAGCAGAGCGAGGATGATGAGCGGTGCTACAGATTCCTTGAAGTGTG 3541
QY 3542 CTACACTACGCTACACTAAGAAAGATTTGATCTGCGCTGCTGCTGCTGCTGCTGCTG 3601
DB 4625 CTACACTACGCTACACTAAGAAAGATTTGATCTGCGCTGCTGCTGCTGCTGCTGCTG 3601
QY 3602 CCTTGGAAAAAGAGTTGGTAGCTTGTATCCGCGCAAAACCAACCGCTGCTGCTGCTG 3661
DB 4565 CCTTGGAAAAAGAGTTGGTAGCTTGTATCCGCGCAAAACCAACCGCTGCTGCTGCTG 3661
QY 3662 GTTTTGTGTTGCAAGCAGAGATTAAGCGGCAAGAAAAAGATCTCAAGAAATCTT 3721
DB 4505 GTTTTGTGTTGCAAGCAGAGATTAAGCGGCAAGAAAAAGATCTCAAGAAATCTT 3721
QY 3722 TGATCTTTCTACAGGGGTCTGACGCTCACTGATGAGCAAGAAATCTCAAGTAAAGATTT 3781
DB 4445 TGATCTTTCTACAGGGGTCTGACGCTCACTGATGAGCAAGAAATCTCAAGTAAAGATTT 3781
QY 3782 TCATGAGATTATC----- 3794
DB 4385 TCATGAGATTATC----- 3794
QY 3795 -----GTGACCA 3802
DB 4325 GCAAGTCAAGTCTGCTCCTCGGCAAGAGTCAAGCTTGCAGCGCGGCTCGCGCA 4266
QY 3803 AAGCGGCAATGCTGCTCCCACTCTGCAAGTTCCGGGGCAGATGATCCGATAGCCGC 3862
DB 4265 GAGCGAACTCCGCGCCCAAGGCTGCTGCGCATCTGCTGATGAGCGCGGCTCGAGGCGCT 4206

QY 3863 TGCTGTTTCTTGATCCGACGGAATTTGACCTGCGGTAGAACTCCGAGTGTCTCA 3922
 Db 4205 CCCGGAAGTTGTGGAACACGACCTCCGACCACTGGGCTTACAGCTCTGTCAGAGCCGCGCA 4146
 QY 3923 GCC----- 3925
 Db 4145 CCCACACCCAGCGCAGGCTGTTGTCGCGCACCACTGGTCTTGACCGCGCTGATGAACA 4086
 QY 3926 ---TCAGCAGCAGGTGAACCACTCCGAGGGGATGACGCCGGGGGTGGCGAAGAACT 3982
 Db 4085 GGGTCAAGTCTCCCGGACACACCGGGGAAGTGTCTTCCACAGAAAGTCCGGGAGAAAC 4026
 QY 3983 CCAGCATG-----AGATCCCGCGCTGAGAGATCATCCAGCCGCGCTC 4025
 Db 4025 CGAGCTGTGCACTTGGCCCATGTGGGCCCTCTCACTGCTATATTAGAAACATTTATC 3966
 QY 4026 CCGGAAAACATTTCCGAAGCCCACTTTCAATAGAAAGCGGGGTGAATCGAAATCTCG 4085
 Db 3965 AGGGTTATTGTCATGAGCGGATACATATTGAATGATTAGAAAAATAAACAAATAG 3906
 QY 4086 TGAATGAGGTTGGGCGTCCGTTGGTGGTCAATTTCCAGCCCGAGATCCCGC----- 4138
 Db 3905 GGGTTCCGCGCAATTTCCCGAAAAGTGCACCTGTATGCGGTGAAATACCGCACAG 3846
 QY 4139 -----TCAGAAAGCTC 4150
 Db 3845 ATGCGTAAGGAGAAATATCCGCATCAGAAATTTGTAACGTTAATTCAGAAAGATC 3786
 QY 4151 GTCAAGAGCGGATAGAAAGCGATGCGCTGCGAATCGGAGCGCGATACCGTTAAAGCAC 4210
 Db 3785 GTCAAGAGCGGATAGAAAGCGATGCGCTGCGAATCGGAGCGCGATACCGTTAAAGCAC 3726
 QY 4211 GAGGAACGGGTGAGCCCATTCGCGGCAAGTCTTTCAAGCAATATCAAGGGTGAAGCAC 4270
 Db 3725 GAGGAACGGGTGAGCCCATTCGCGGCAAGTCTTTCAAGCAATATCAAGGGTGAAGCAC 3666
 QY 4271 TATGCTGATAGGCGTCCGCGCACACCGCGGCGCAAGTCAATGATCCAGAAAAGCG 4330
 Db 3665 TATGCTGATAGGCGTCCGCGCACACCGCGGCGCAAGTCAATGATCCAGAAAAGCG 3606
 QY 4331 GCCATTTTCCACCATGATATTTCGCAAGCAGCATTCGCTCAAGAGATCTTC 4390
 Db 3605 GCCATTTTCCACCATGATATTTCGCAAGCAGCATTCGCTCAAGAGATCTTC 3546
 QY 4391 GCGGTGGGATGCGGCGCTTTGAGCTGCGGGAAGATTCGCTGCGCGAGCCCTGATG 4450
 Db 3545 GCGGTGGGATGCGGCGCTTTGAGCTGCGGGAAGATTCGCTGCGCGAGCCCTGATG 3486
 QY 4451 CTCTTGGTCAGATCATCTGATCGACAGACCGGCTTCATCCGATAGTGTGCTGCTC 4510
 Db 3485 CTCTTGGTCAGATCATCTGATCGACAGACCGGCTTCATCCGATAGTGTGCTGCTC 3426
 QY 4511 GATGCAATGTTTGGCTTGTGTCGATGGAATGGGAGTAGCCGATCAAGCCTATGACCG 4570
 Db 3425 GATGCAATGTTTGGCTTGTGTCGATGGAATGGGAGTAGCCGATCAAGCCTATGACCG 3366
 QY 4571 CCGCATTTGATCAGCCATGATGATATTCTTCTGCGCAGAGCAAGGTGAATGACAGAG 4630
 Db 3365 CCGCATTTGATCAGCCATGATGATATTCTTCTGCGCAGAGCAAGGTGAATGACAGAG 3306
 QY 4631 ATCTGCGCGGACATTCGCGCAATAGCAGCAGTCCCTCCGCGTTCACTGACCAAGTTC 4690
 Db 3305 ATCTGCGCGGACATTCGCGCAATAGCAGCAGTCCCTCCGCGTTCACTGACCAAGTTC 3246
 QY 4691 GAGCAGAGCTGCGCAAGGAACGCCCGTGTGCGCAGCAGATAGCCGCTGCTGCTC 4750
 Db 3245 GAGCAGAGCTGCGCAAGGAACGCCCGTGTGCGCAGCAGATAGCCGCTGCTGCTC 3186
 QY 4751 CTGCAATTTTCAAGGCAACCGGACAGAGTGGTCTTGAACAAAAAGAACCGGGGCGCTTG 4810
 Db 3185 TTGCAATTTTCAAGGCAACCGGACAGAGTGGTCTTGAACAAAAAGAACCGGGGCGCTTG 3126

QY 4811 CGTGAACCGCGGAACAAGCGCGCATCAGACAGCCGATGCTGTTGTCAGATCA 4870
 Db 3125 CGTGAACCGCGGAACAAGCGCGCATCAGACAGCCGATGCTGTTGTCAGATCA 3066
 QY 4871 GCCGAATAGCCTCTCCACCCAGCGGCGGAGAACTGCGTGAATCCATCTTGTCAAT 4930
 Db 3065 GCCGAATAGCCTCTCCACCCAGCGGCGGAGAACTGCGTGAATCCATCTTGTCAAT 3006
 QY 4931 CATGCGAAAGATTCCTCATCTGCTCTTGTATCAGATCTTGAATCCCTGCGCCATCAGAT 4990
 Db 3005 CATGCGAAAGATTCCTCATCTGCTCTTGTATCAGATCTTGAATCCCTGCGCCATCAGAT 2946
 QY 4991 CTTGGCGGCAAGAAAGCCATCCAGTTTATCTTGCAGGCGCTTCCCACTTAACAGAGGG 5050
 Db 2945 CTTGGCGGCAAGAAAGCCATCCAGTTTATCTTGCAGGCGCTTCCCACTTAACAGAGGG 2886
 QY 5051 CGCCCAAGCTGGCAATTCGCGTTCGTTGTCATTAACCGCCAGTCACTATCG 5110
 Db 2885 CGCCCAAGCTGGCAATTCGCGTTCGTTGTCATTAACCGCCAGTCACTATCG 2826
 QY 5111 CCATGTAAGCCCACTGCAAGCTACTGCTTCTTCTTGGCGCTTTCCTTGTCCA 5170
 Db 2825 CCATGTAAGCCCACTGCAAGCTACTGCTTCTTCTTGGCGCTTTCCTTGTCCA 2766
 QY 5171 GATGAGCCAGTGAAGTCAATTCATCCGAGGTCAGACCGTTTTCGCGGACTGCTTCTA 5230
 Db 2765 GATGAGCCAGTGAAGTCAATTCATCCGAGGTCAGACCGTTTTCGCGGACTGCTTCTA 2706
 QY 5231 CGTG 5234
 Db 2705 CGTG 2702

RESULT 3
 US-10-517-698-1/c
 ; Sequence 1, Application US/10517698
 ; Publication No. US20060068390A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tiller et al.
 ; TITLE OF INVENTION: DNA AMPLIFICATION AND SEQUENCING IN COLLAPSIBLE EMULSIONS
 ; FILE REFERENCE: 23004/40746
 ; CURRENT APPLICATION NUMBER: US/10/517,698
 ; PRIORITY FILING DATE: 2004-12-13
 ; PRIOR APPLICATION NUMBER: PCT/AU03/00746
 ; PRIORITY FILING DATE: 2003-06-13
 ; PRIOR APPLICATION NUMBER: AU PS 2981
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 4245
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Plasmid pCR-BIunt II-TOPO
 US-10-517-698-1

Query Match 30.9%; Score 1634.4; DB 13; Length 4245;
 Best Local Similarity 80.6%; Pred. No. 0;
 Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3;

QY 2942 CTTCCGCTTCTGCTCACTGATCGCTGCGTCTGTTGCGGTCGCGGAGCGGTAT 3001
 Db 4245 CTTCCGCTTCTGCTCACTGATCGCTGCGTCTGTTGCGGTCGCGGAGCGGTAT 4186
 QY 3002 CAGCTCACTCAAGGCGGTAAATACGTTATCCACAGATCAAGGGAATTAACGAGAAAGA 3061
 Db 4185 CAGCTCACTCAAGGCGGTAAATACGTTATCCACAGATCAAGGGAATTAACGAGAAAGA 4126
 QY 3062 ACATGTGACAAAGGCGCAGCAAAAGCGCAGAAACGTAATAAGGCGCGTGTGCGCT 3121
 Db 4125 ACATGTGACAAAGGCGCAGCAAAAGCGCAGAAACGTAATAAGGCGCGTGTGCGCT 4066

Db 1905 CCTGGCGGCGAAGAAACCATCACTTACCTTTCAGAGGGCTTCCAACTTACAGAGAGG 1846
Qy 5051 CGCCCCAGCTGGCAATTCGGGTTCCGTTCTGTCTCATATAAACCGCCCACTAGCTATCG 5110
Db 1845 CGCCCCAGCTGGCAATTCGGGTTCCGTTCTGTCTCATATAAACCGCCCACTAGCTATCG 1786
Qy 5111 CCATGTAAAGCCCACTGCAAGCTACTGCTTTCTCTTTGGCTTGGCTTTCCCTTGTCCA 5170
Db 1785 CCATGTAAAGCCCACTGCAAGCTACTGCTTTCTCTTTGGCTTGGCTTTCCCTTGTCCA 1726
Qy 5171 GATAGCCAGTAGTACGATTCATCCGGGGTCAGACCGTTTCTCCGAGCTGGCTTTCTTA 5230
Db 1725 GATAGCCAGTAGTACGATTCATCCGGGGTCAGACCGTTTCTCCGAGCTGGCTTTCTTA 1666
Qy 5231 CGTG 5234
Db 1665 CGTG 1662

RESULT 4
US-11-193-750-10/c
; Sequence 10, Application US/11193750
; Publication No US20050273873A1
; GENERAL INFORMATION:
; APPLICANT: Avigenics, Inc
; TITLE OF INVENTION: MODIFICATION OF THE GENOME BY INTRODUCTION OF LARGE NUCLEIC ACID
; FILE REFERENCE: AVI-025CIP4
; CURRENT APPLICATION NUMBER: US/11/193,750
; PRIORITY FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/11/068,155
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 6233
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid PCR-XL-TOPO-CMV-pur-atcb
US-11-193-750-10

Query Match 30.9%; Score 1634.4; DB 17; Length 6233;
Best Local Similarity 80.6%; Pred. No. 0;
Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3;

Qy 2942 CTTCCGCTTCTCGCTCACTACCTCGCTGCGCTGCTGCTGCTGCGGAGCGGTAT 3001
Db 6233 CTTCCGCTTCTCGCTCACTACCTCGCTGCGCTGCTGCTGCTGCGGAGCGGTAT 6174
Qy 3002 CAGCTCACTCAAAAGCGGTATACGTTATCCAGAGATCAGGGGATTAAGCAGAGAAAG 3061
Db 6173 CAGCTCACTCAAAAGCGGTATACGTTATCCAGAGATCAGGGGATTAAGCAGAGAAAG 6114
Qy 3062 ACATGTAGCAAAAGGCGCAGCAAAAGGCGAGAAACCGTAAAAAAGCGCGCTTGTGCGCT 3121
Db 6113 ACATGTAGCAAAAGGCGCAGCAAAAGGCGAGAAACCGTAAAAAAGCGCGCTTGTGCGCT 6054
Qy 3122 TTTTCCATAGGCTCCGCCCCCTTCAAGCATCACAAAATTCAGCGCTCAAGTCAAGGT 3181
Db 6053 TTTTCCATAGGCTCCGCCCCCTTCAAGCATCACAAAATTCAGCGCTCAAGTCAAGGT 5994
Qy 3182 GGGCAACCCGACAGAGATTAAGATACAGGGGTTTCCCGTGAAGCTCCCTGCTGC 3241
Db 5993 GGGCAACCCGACAGAGATTAAGATACAGGGGTTTCCCGTGAAGCTCCCTGCTGC 5994
Qy 3242 GCTTCCTGTTCCAGACCTTCGCTTACCGGATACCTGCGCTTTCTCCCTTCGGGAA 3301
Db 5933 GCTTCCTGTTCCAGACCTTCGCTTACCGGATACCTGCGCTTTCTCCCTTCGGGAA 5874
Qy 3302 GCGTGGGCTTTTCTCATAGCTCAAGCTGTAGTATCTCAGTTCGGTGTAGGTGCTTGGCT 3361
Db 5873 GCGTGGGCTTTTCTCATAGCTCAAGCTGTAGTATCTCAGTTCGGTGTAGGTGCTTGGCT 5814

Qy 3362 CCAAGCTGGGCTGTGTGACAGAAACCCCGTTACAGCCCGACCGCTGCGCTTATCCGGTA 3421
Db 5813 CCAAGCTGGGCTGTGTGACAGAAACCCCGTTACAGCCCGACCGCTGCGCTTATCCGGTA 5754
Qy 3422 ACTATCGTCTTGAAGTCCAAACCGGTAAAGACAAGATTATGCGCACTGGCAGACGCACTG 3481
Db 5753 ACTATCGTCTTGAAGTCCAAACCGGTAAAGACAAGATTATGCGCACTGGCAGACGCACTG 5694
Qy 3482 GTAACAGATTATGACAGACCGAGATATGTAAGCGGTGTCAAGAGTTCTTGAAGTGTGGC 3541
Db 5693 GTAACAGATTATGACAGACCGAGATATGTAAGCGGTGTCAAGAGTTCTTGAAGTGTGGC 5634
Qy 3542 CTAATACGGCTACACTGAGAAACAAGATTATGATGTGGCTCTGTGTAAGCAGTTA 3601
Db 5633 CTAATACGGCTACACTGAGAAACAAGATTATGATGTGGCTCTGTGTAAGCAGTTA 5574
Qy 3602 CTTTCGAAAAAGATTGTAAGTCTTGATCCGCAACAAACACACGCTGTAGCGGTG 3661
Db 5573 CTTTCGAAAAAGATTGTAAGTCTTGATCCGCAACAAACACACGCTGTAGCGGTG 5514
Qy 3662 GTTTTTTTTGTTCAGACAGCATTTACGCGCAGAAAAAGATCTCAAGAGATCTT 3721
Db 5513 GTTTTTTTTGTTCAGACAGCATTTACGCGCAGAAAAAGATCTCAAGAGATCTT 5454
Qy 3722 TGATCTTTTCTACAGGGGTCTGAGCTCAGTGAAGAAAGAAATCAGCTTAAGGATTTTG 3781
Db 5453 TGATCTTTTCTACAGGGGTCTGAGCTCAGTGAAGAAAGAAATCAGCTTAAGGATTTTG 5394
Qy 3782 TCATGAGATTATC----- 3794
Db 5393 TCATGAGATTATCAAAAAAGATCTTCACTAGATCCTTTAATTAATAAGATTTTA 5334
Qy 3795 -----GTGACCA 3802
Db 5333 GCAAGTGTACGTCTGTCTCTGCGCAAGATGACAGCATTTGCCGCGCGCGCA 5274
Qy 3803 AAGCGGCATGATGTCCTCCCACTCTGCAAGTTGGGGGACATGATGGCGGATAGCGCGC 3862
Db 5273 GGGGAACTCCCGCCCCCAGGCTGTGCGCGATCTGCGTATGCGCGGCCGAGAGGCT 5214
Qy 3863 TGTGTGTTTCTGTGATCCGACGAGATTGCACTGCGCGGTAGAACTCCGCGAGTCTGCA 3922
Db 5213 CCGGGAAGTTGTGTGACACGACCTCGACCACTCGGGGTACAGTCTGTCCAGCGCGCA 5154
Qy 3923 GCC----- 3925
Db 5153 CCGACACCCAGGCGAGGTGTGTCGCGACCACTGTGCTGTGACCGCGCTGATGAACA 5094
Qy 3926 ---TCAGGACAGAGCTGAACCACTGCGGAGGGATGAGACCGGGGTGGCGGAAGACT 3982
Db 5093 GGGTCACTGTGTCGCGACCACTCGGGAAGTGTCTTCCAGAAATCCCGGAGAAC 5034
Qy 3983 CAGCATGAGATCCCGCGCTGAGGATTCATCCAGCGCGGTCCCGGAAAAAGATTCCGA 4042
Db 5033 CAGCGCGGTGTGACAACTCGACCGCTCCGCGAGAGTGTGCGCGGTGAGCACCGGAA 4974
Qy 4043 AGCCCAACTTTATATAGAGCGCGGTGAATTCGAAATCTGTGATGAGAGTGGCG 4102
Db 4973 CCGGACTGTGCACTTGGCCATGTGGCTCTCTCACTGTCTATTTGAAGCAATTATC 4914
Qy 4103 TCGCTGTGTGCTTATTCGACCCAGAGTCCCG----- 4137
Db 4913 AGGGTATGTCTCATAGAGCGGATCATTTTAATTAAGAAAAATAACAAATAG 4854
Qy 4138 ----- 4137
Db 4853 GGGTTCGCGCACATTTCCCGAAAGTGCACCTGTATGCGGTGTGAATTAACGACAG 4794
Qy 4138 -----CTCAGAAAGATC 4150
Db 4793 ATGCGTAAGAGAAAAATACCGCATCAGAAATTGTAAAGCTTAATTAATCAGAAAGATC 4734

QY 4151 GTCAAGAGGCGATAGAGGCGATGCGCTGCGAATCGGGAAGCGCGGATACCGTAAAGCAC 4210
DB 4733 GTCAAGAGGCGATAGAGGCGATGCGCTGCGAATCGGGAAGCGCGGATACCGTAAAGCAC 4674
QY 4211 GAGGAAGCGGTCAAGCCGATTCGCGGCAAGCTCTTCAGCAATACAGGGTAGCCAAAGC 4270
DB 4673 GAGGAAGCGGTCAAGCCGATTCGCGGCAAGCTCTTCAGCAATACAGGGTAGCCAAAGC 4614
QY 4271 TAGTCTGTAAGCGGTCCGCGACACCGGCGGCAAGCTCGATGTAATCCAGAAAAGCG 4330
DB 4613 TAGTCTGTAAGCGGTCCGCGACACCGGCGGCAAGCTCGATGTAATCCAGAAAAGCG 4554
QY 4331 GCCATTTTCCACCATGATATTCGCGCAAGCGGATGCGCATGGGTTCAGAGAGATCTTC 4390
DB 4553 GCCATTTTCCACCATGATATTCGCGCAAGCGGATGCGCATGGGTTCAGAGAGATCTTC 4494
QY 4391 GCGGTGCGGCGATGCGCGCTTGAGCCCTGCGAAAGTTTCGCTGCGCGAGCCCTGATG 4450
DB 4493 GCGGTGCGGCGATGCGCGCTTGAGCCCTGCGAAAGTTTCGCTGCGCGAGCCCTGATG 4434
QY 4451 CTCTTCTCCAGATCATCTGATGATGACAAAGCCGGCTTCCATCCGATGATGCTGCTC 4510
DB 4433 CTCTTCTCCAGATCATCTGATGATGACAAAGCCGGCTTCCATCCGATGATGCTGCTC 4374
QY 4511 GATGCGATGTTTGGCTTGTGTGTAATGGGCAAGTACCGGATCCAGGCTATGCGAGCG 4570
DB 4373 GATGCGATGTTTGGCTTGTGTGTAATGGGCAAGTACCGGATCCAGGCTATGCGAGCG 4314
QY 4571 CCGCATTTGATCAAGCCATGATGATCTTTCTCGGCAAGCAAGGTGAGATGACAGAG 4630
DB 4313 CCGCATTTGATCAAGCCATGATGATCTTTCTCGGCAAGCAAGGTGAGATGACAGAG 4254
QY 4631 ATCTGCGCGCGGCACTTGGCGCAATAGACAGCTCCCTCCGCTTCACTGCAAGCTC 4690
DB 4253 ATCTGCGCGCGGCACTTGGCGCAATAGACAGCTCCCTCCGCTTCACTGCAAGCTC 4194
QY 4691 GAGCAGAGCTGCGCAAGAAAGCCCGCTGCGCAAGCAGATAGCGCGCTGCTGCTC 4750
DB 4193 GAGCAGAGCTGCGCAAGAAAGCCCGCTGCGCAAGCAGATAGCGCGCTGCTGCTC 4134
QY 4751 CTGCAAGTTCACTCAAGGCGACCGGACAGGTGCTTTGACAAAAGAAACCGGAGCGCCCTG 4810
DB 4133 TTGCAAGTTCACTCAAGGCGACCGGACAGGTGCTTTGACAAAAGAAACCGGAGCGCCCTG 4074
QY 4811 CGCTGACAGCGCGGAAACAGCGCGGATTCAGAGCAGCGATGTTCTGTTTGGCCAGTATC 4870
DB 4073 CGCTGACAGCGCGGAAACAGCGCGGATTCAGAGCAGCGATGTTCTGTTTGGCCAGTATC 4014
QY 4871 GCCGAATAGCTCTCAAGCCCAAGCGGCGGAGAACTGCGTGAATTCATCTTGTCAAT 4930
DB 4013 GCCGAATAGCTCTCAAGCCCAAGCGGCGGAGAACTGCGTGAATTCATCTTGTCAAT 3954
QY 4931 CATGCAAAAGATCTTCATCTGCTCTTGTATCAGATCTTGAATCCCTGCGCATCAGAT 4990
DB 3953 CATGCAAAAGATCTTCATCTGCTCTTGTATCAGAGCTTGAATCCCTGCGCATCAGAT 3894
QY 4991 CCTTGGCGGCAAGAAAGCCATTCAGTTTACTTTGCAAGGGTTCCCAACTTACCAAGGG 5050
DB 3893 CCTTGGCGGCAAGAAAGCCATTCAGTTTACTTTGCAAGGGTTCCCAACTTACCAAGGG 3834
QY 5051 CGCCCAAGCTGCAATTCGCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5110
DB 3833 CGCCCAAGCTGCAATTCGCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3774
QY 5111 CCATGTAAGCCCACTGCAAGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 5170
DB 3773 CCATGTAAGCCCACTGCAAGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 3714
QY 5171 GATAGCCAGTACTGATGATTCATTCGCGGGGTGAGCAAGCTTTCGCGGAGTGGCTTCTCA 5230
DB 3713 GATAGCCAGTACTGATGATTCATTCGCGGGGTGAGCAAGCTTTCGCGGAGTGGCTTCTCA 3654
QY 5231 CGTG 5234

DB 3653 CGTG 3650
RESULT 5
US-10-764-818A-11
; Sequence 11, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVIATIS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CULI
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10764,818A
; CURRENT FILING DATE: 2004-01-26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the HV-GHRH plasmid.
US-10-764-818A-11
Query Match 30.4%; Score 1603.8; DB 11; Length 3534;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;
QY 2706 CTAGAGTATATCATAGTATAGCTGTTTCTGTGTGAATGTTATCCGCTCAATTCG 2765
DB 1412 CTGGGCTATATCATAGTATAGCTGTTTCTGTGTGAATGTTATCCGCTCAATTCG 1471
QY 2766 ACAACAATATGAGAGCGGAGCAATAAAGTAAAGCTGAGGCTGCTTAATGATGAGCTA 2825
DB 1472 ACAACAATATGAGAGCGGAGCAATAAAGTAAAGCTGAGGCTGCTTAATGATGAGCTA 1531
QY 2826 ACTCAATATATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2885
DB 1532 ACTCAATATATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1591
QY 2886 GCTGCAATATATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2945
DB 1592 GCTGCAATATATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1651
QY 2946 CGCTTCTGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3005
DB 1652 CGCTTCTGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1711
QY 3006 TCATCTAAAGGGGCTTAATCGGTTATCCACAAATACAGGAGTAACGCAAGAAAGAAACAT 3065
DB 1712 TCATCTAAAGGGGCTTAATCGGTTATCCACAAATACAGGAGTAACGCAAGAAAGAAACAT 1771
QY 3066 GTGAGCAAAAGGCGCAGCAAAAGGCGTAAAGGCGGCGCTTGTGCGGCTTTT 3125
DB 1772 GTGAGCAAAAGGCGCAGCAAAAGGCGTAAAGGCGGCGCTTGTGCGGCTTTT 1831
QY 3126 CCATAGGCTCCGCGCCCTTGAAGCATCAAAAATGACGCTCAAGTCAAGTGGCGG 3185
DB 1832 CCATAGGCTCCGCGCCCTTGAAGCATCAAAAATGACGCTCAAGTCAAGTGGCGG 1891
QY 3186 AAAACCGAGAGACTTAATGAATACAGGCGTTTCCCTGGAAGCTCCCTGCGGCTC 3245
DB 1892 AAAACCGAGAGACTTAATGAATACAGGCGTTTCCCTGGAAGCTCCCTGCGGCTC 1951
QY 3246 TCTGTTCCGAGCTGCGCTTACCGGATACCTGTCGCTTCTTCTTCCGGAAGCGT 3305
DB 1952 TCTGTTCCGAGCTGCGCTTACCGGATACCTGTCGCTTCTTCTTCCGGAAGCGT 2011
QY 3306 GGGGCTTCTCATAGTCAAGCTGATGATCTCAGTTGCGGTGAGTGGTTCGCTCA 3365
DB 2012 GGGGCTTCTCATAGTCAAGCTGATGATCTCAGTTGCGGTGAGTGGTTCGCTCA 2071

QY 3366 GCTGGGCTGTGTGACGAAACCCCGCTTCAAGCCGACCGCTGCGCTTATCCGGTAACATA 3425
Db 2072 GCTGGGCTGTGTGACGAAACCCCGCTTCAAGCCGACCGCTGCGCTTATCCGGTAACATA 2131
QY 3426 TCGTCTTGAAGTCCAAACCGGTAAGACACGACTTATCCGCACTGGACAGCACTGGTAA 3485
Db 2132 TCGTCTTGAAGTCCAAACCGGTAAGACACGACTTATCCGCACTGGACAGCACTGGTAA 2191
QY 3486 CAGGATTAGCAGAGCGAGTATGTAGGCGGCTTACAGAGTCTTGAAGTGGTCCCTAA 3545
Db 2192 CAGGATTAGCAGAGCGAGTATGTAGGCGGCTTACAGAGTCTTGAAGTGGTCCCTAA 2251
QY 3546 CTACGGCTACACTAGAAAGACATATTTGATCTGCGCTGCTGTAAGCCAGTAACTT 3605
Db 2252 CTACGGCTACACTAGAAAGACATATTTGATCTGCGCTGCTGTAAGCCAGTAACTT 2311
QY 3606 CGGAAAAAGAGTGTAGCTTTGATCCGGCAAAACCAACCGCTGGTAGCGGTGTT 3665
Db 2312 CGGAAAAAGAGTGTAGCTTTGATCCGGCAAAACCAACCGCTGGTAGCGGTGTT 2371
QY 3666 TTTTGTTCGAAAGCAGAGTATGCGCGCAAAAAAGATCTGAAAGATCCCTTGAT 3725
Db 2372 TTTTGTTCGAAAGCAGAGTATGCGCGCAAAAAAGATCTGAAAGATCCCTTGAT 2431
QY 3726 CTTTCTTACCGGGGTCTGACGCTCAGTGGAAAGAAACTCAGTAAAGGATTTGTGAT 3785
Db 2432 CTTTCTTACCGGGGTCTGACGCTCAGTGGAAAGAAACTCAGTAAAGGATTTGTGAT 2449
QY 3786 GAGATTATCGTCAACCAAGCGGCAATGTCCTCCCACTCTGCAAGTTGCGGGGCAATG 3845
Db 2449 GAGATTATCGTCAACCAAGCGGCAATGTCCTCCCACTCTGCAAGTTGCGGGGCAATG 2449
QY 3846 GATGCGGGAATAGCGCGTGTGTTTCTGTGATCCGACGATTTGCACTGCCGTAGAA 3905
Db 2450 GATGCGGGAATAGCGCGTGTGTTTCTGTGATCCGACGATTTGCACTGCCGTAGAA 2449
QY 3906 CTCGCGAGGTGCTCAAGCTCAGGACAGAGTGAACCACTCGGAGGGATGAGGCC 3965
Db 2450 CTCGCGAGGTGCTCAAGCTCAGGACAGAGTGAACCACTCGGAGGGATGAGGCC 2449
QY 3966 GGGGTGGCGAAGATCTCAGCATGAGATCCCGCGCTGAGAGATCATCCAGCGGCGTC 4025
Db 2450 GGGGTGGCGAAGATCTCAGCATGAGATCCCGCGCTGAGAGATCATCCAGCGGCGTC 2449
QY 4026 CCGGAAAAAGATTCGGAAGCCCACTTTCATAGAAAGCGCGGTGAATCGAAATCTCG 4085
Db 2450 CCGGAAAAAGATTCGGAAGCCCACTTTCATAGAAAGCGCGGTGAATCGAAATCTCG 2449
QY 4086 TGATGCGAGGTGGCGTCTGCTGTGTCATTTGCAACCCAGAGTCCCGCTCAGAG 4145
Db 2450 TGATGCGAGGTGGCGTCTGCTGTGTCATTTGCAACCCAGAGTCCCGCTCAGAG 2459
QY 4146 AACTCGTCAAGAAAGCGATGAAAGCGATGCGTTCGCAATCCGAGCGCGATACCGTAA 4205
Db 2460 AACTCGTCAAGAAAGCGATGAAAGCGATGCGTTCGCAATCCGAGCGCGATACCGTAA 2519
QY 4206 AGCAGAGGAAGGGGTAGGCGCAATTCGCGCAAGCTTTCAGAAATATCAAGGTAGCC 4265
Db 2520 AGCAGAGGAAGGGGTAGGCGCAATTCGCGCAAGCTTTCAGAAATATCAAGGTAGCC 2579
QY 4266 AAGCGTATGTCTGATAGCGGTCCGACACCCAGCGGCGCAAGTGAATCCAGAA 4325
Db 2580 AAGCGTATGTCTGATAGCGGTCCGACACCCAGCGGCGCAAGTGAATCCAGAA 2639
QY 4326 AAGCGGCAATTTTCCACATGATATTCGCAAGAGGCAATGCCATGGTCAACAGAGA 4385
Db 2640 AAGCGGCAATTTTCCACATGATATTCGCAAGAGGCAATGCCATGGTCAACAGAGA 2699
QY 4386 TCCGCGCGGTGCGGCAATGCGGCGCTTGAAGCGGCAAGTTCGCTGGCGGAGGCC 4445
Db 2700 TCCGCGCGGTGCGGCAATGCGGCGCTTGAAGCGGCGCTTGAAGCGGCGGAGGCC 2759
QY 4446 TGATGCTCTTCTGTCAGATCATCTGATCGAACAGACCGGCTTCATCCAGTACGTGCT 4505

Db 2760 TGATGCTCTTCTGTCAGATCATCTGATCGAACAGACCGGCTTCATCCAGTACGTGCT 2819
QY 4506 CGCTGATGCGATGTTTCCGCTGTTGTCGATAGGCGAGTACCGGATCAAGCGTATGC 4565
Db 2820 CGCTGATGCGATGTTTCCGCTGTTGTCGATAGGCGAGTACCGGATCAAGCGTATGC 2879
QY 4566 AGCGCGCGCAATTTGATAGCGCATGAGTATCTTCTCGGAGAGAGCAAGGTGAGTAC 4625
Db 2880 AGCGCGCGCAATTTGATAGCGCATGAGTATCTTCTCGGAGAGAGCAAGGTGAGTAC 2939
QY 4626 AGGATCTTCCGCGCACTTCCGCAATAGCAGAGTCCCTCCGCTTCAAGTACA 4685
Db 2940 AGGATCTTCCGCGCACTTCCGCAATAGCAGAGTCCCTCCGCTTCAAGTACA 2999
QY 4686 AGTGAAGCAGCTGCGCAAGAAACCGGCTGTCGCGCAGCAGATAGCGCGTGC 4745
Db 3000 AGTGAAGCAGCTGCGCAAGAAACCGGCTGTCGCGCAGCAGATAGCGCGTGC 3059
QY 4746 TCGTCTGCAAGTTCATTCAGGCGCACCGGACAGGTGCGTTCGAAAGAAACCGGCGC 4805
Db 3060 TCGTCTGCAAGTTCATTCAGGCGCACCGGACAGGTGCGTTCGAAAGAAACCGGCGC 3119
QY 4806 CCTGCGCTGACAGCGCGCAACAGCGCGCATCAGAGCGCATGCTGTTGTCAG 4865
Db 3120 CCTGCGCTGACAGCGCGCAACAGCGCGCATCAGAGCGCATGCTGTTGTCAG 3179
QY 4866 TCATAGCGCAATAGCTTCTCCACCCAGAGCGCGGAGAACCTGTCGATCATCTTGT 4925
Db 3180 TCATAGCGCAATAGCTTCTCCACCCAGAGCGCGGAGAACCTGTCGATCATCTTGT 3239
QY 4926 TCATAGCGCAATAGCTTCTCCACCCAGAGCGCGGAGAACCTGTCGATCATCTTGT 4985
Db 3240 TCATAGCGCAATAGCTTCTCCACCCAGAGCGCGGAGAACCTGTCGATCATCTTGT 3299
QY 4986 CAGATCTTGGCGCAAGAAAGCATGCAATTTTCAAGGAGCTTCCCACTTACA 5045
Db 3300 CAGATCTTGGCGCAAGAAAGCATGCAATTTTCAAGGAGCTTCCCACTTACA 3359
QY 5046 GAGGCGCGCCCAAGTGGCAATTCGAGTTCGCTGTCGATCAATAAACCGCGCATGAC 5105
Db 3360 GAGGCGCGCCCAAGTGGCAATTCGAGTTCGCTGTCGATCAATAAACCGCGCATGAC 3419
QY 5106 TATCGCATGTAAGCCCACTGCAAGTACCTGCTTCTT 5146
Db 3420 TATCGCATGTAAGCCCACTGCAAGTACCTGCTTCTT 3460

RESULT 6
US-10-764-818A-12
; Sequence 12, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OR INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CULI
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10764,818A
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the TI-GHRH plasmid.
US-10-764-818A-12

Query Match 30.4%; Score 1603.8; DB 11; Length 3534;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

Db 3180 TCATAGCCGAATAGCCTCTCCACCCAGCGCGGAGAACTGCGTGAATCATCTTGT 3239
Qy 4926 TCATCATGCGCAAGCATCTCATCTGCTCTGATGAGATCTGATCCCTGCGCAT 4985
Db 3240 TCATCATGCGCAAGCATCTCATCTGCTCTGATGAGATCTGATCCCTGCGCAT 3299
Qy 4986 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGACGGGCTTCCCACTTACCA 5045
Db 3300 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGACGGGCTTCCCACTTACCA 3359
Qy 5046 GAGGCGCGCCCAAGCTGGCAATTCGCGTTCCTGCTGCTCATTAACCGCCAGTCTAGC 5105
Db 3360 GAGGCGCGCCCAAGCTGGCAATTCGCGTTCCTGCTGCTCATTAACCGCCAGTCTAGC 3419
Qy 5106 TATGCGCATGTAGCCCACTGCAAGCTACCTGCTTCTCTT 5146
Db 3420 AACTGTTGGAAAGGCGCATCGGTGCGGCGCTTCTGCTATT 3460

RESULT 7
US-10-764-818A-13
; Sequence 13, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVANIS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUI
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10764, 818A
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent version 3.1
; SEQ ID NO 13
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acid sequence for the TV-GHRH plasmid.
US-10-764-818A-13

Query Match 30.4%; Score 1603.8; DB 11; Length 3534;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 202; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

Qy 2706 CTAGAGCTAATCATGCTCATGCTGCTTCTCTGTAATTTGTTATCGCTCACAATTC 2765
Db 1412 CTGGCGTAATCATGCTCATGCTGCTTCTCTGTAATTTGTTATCGCTCACAATTC 1471
Qy 2766 ACAACAATAGAGCCGGAAGCATTAAGTGAAGCTGGGGTCTCTAATGAGTGA 2825
Db 1472 ACAACAATAGAGCCGGAAGCATTAAGTGAAGCTGGGGTCTCTAATGAGTGA 1531
Qy 2826 ACTCACTTAATGCTGCTGCTCACTGCGCTTTTCCAGTCGGGAAACCTGTCTGCCA 2885
Db 1532 ACTCACTTAATGCTGCTGCTCACTGCGCTTTTCCAGTCGGGAAACCTGTCTGCCA 1591
Qy 2886 GCTGCAATTAATGATCGGCGCAAGCGCGGGGAGAGGCGGTTTGGGTATGGGCCCTCTTC 2945
Db 1592 GCTGCAATTAATGATCGGCGCAAGCGCGGGGAGAGGCGGTTTGGGTATGGGCCCTCTTC 1651
Qy 2946 CGCTTCTCTGCTCACTGCTGCTGCGCTGCTGCTTCCGCTGCGGAGAGCGGTATCAGC 3005
Db 1652 CGCTTCTCTGCTCACTGCTGCTGCGCTGCTGCTTCCGCTGCGGAGAGCGGTATCAGC 1711
Qy 3006 TCACCTCAAGCGGTAATACGCTTATCCAGAAATCAGGGGATTAACGAGAAAGAAAT 3065
Db 1712 TCACCTCAAGCGGTAATACGCTTATCCAGAAATCAGGGGATTAACGAGAAAGAAAT 1771
Qy 3066 GTGAGCAAAAGGCGAGAAAGCGCAAGAACCGTAAAGAGCGCGCTGCTGGGTTT 3125
Db 1772 GTGAGCAAAAGGCGAGAAAGCGCAAGAACCGTAAAGAGCGCGCTGCTGGGTTT 1831
Qy 3126 CATTAGGCTCGCCCGCTGAGCATCAAAAAATCGACGCTCAAGTCAAGAGTGGCG 3185

Db 1832 CCATAGGCTCGCCCGCTGAGAGCATCAAAAAATGAGGCTCAATCAGAGGTGCG 1891
Qy 3186 AAACCCGACAGACTATTAAGATACAGGCGTTTCCCTGGAAGCTCCTGTGCGCTC 3245
Db 1892 AAACCCGACAGACTATTAAGATACAGGCGTTTCCCTGGAAGCTCCTGTGCGCTC 1951
Qy 3246 TCGTGTCCGACCGTGGCGCTTACCGGATACCTGTCCGCTTCTCCCTTGGGAAAGGT 3305
Db 1952 TCGTGTCCGACCGTGGCGCTTACCGGATACCTGTCCGCTTCTCCCTTGGGAAAGGT 2011
Qy 3306 GCGCGTTTCTATAGCTCACGCTGTAGGTATCTGAGTTGCGTGTAGTGTGCTGCCAA 3365
Db 2012 GCGCGTTTCTATAGCTCACGCTGTAGGTATCTGAGTTGCGTGTAGTGTGCTGCCAA 2071
Qy 3366 GCTGGGCTGTGTGACAGAACCCCGCTTACGCGGACCGCTGCGCTTATCCGTA 3425
Db 2072 GCTGGGCTGTGTGACAGAACCCCGCTTACGCGGACCGCTGCGCTTATCCGTA 2131
Qy 3426 TCGTGTGAGTCCAAACCGGTAAGACAGACTTATCCGCTGAGAGAGCACTGTGTA 3485
Db 2132 TCGTGTGAGTCCAAACCGGTAAGACAGACTTATCCGCTGAGAGAGCACTGTGTA 2191
Qy 3486 CAGGATTAGCAGAGCGAGTATGTAGCGGCTGCTACAGAGTTCTTGAAGTGTGCGCTAA 3545
Db 2192 CAGGATTAGCAGAGCGAGTATGTAGCGGCTGCTACAGAGTTCTTGAAGTGTGCGCTAA 2251
Qy 3546 CTACGCTACACTAGAAAGAACAGTATTTGTATGCTGCTGCTGTAAGCCAGTTACCTT 3605
Db 2252 CTACGCTACACTAGAAAGAACAGTATTTGTATGCTGCTGCTGTAAGCCAGTTACCTT 2311
Qy 3606 CGGAAAAAGGTGTGTGCTTGTATCCGGAACCAACCGCTGTAGCGGTGTT 3665
Db 2312 CGGAAAAAGGTGTGTGCTTGTATCCGGAACCAACCGCTGTAGCGGTGTT 2371
Qy 3666 TTTTGTGCAAGCAGAGATTAAGCGCAGAAAAAGATCTCAAGAAAGTCTTTGAT 3725
Db 2372 TTTTGTGCAAGCAGAGATTAAGCGCAGAAAAAGATCTCAAGAAAGTCTTTGAT 2431
Qy 3726 CTTTGTACGCGGCTGTGACGCTCAGTGAAGAAACTCACTTGAAGGATTTTGTAT 3785
Db 2432 CTTTGTACGCGGCTGTGACGCTCAGTGAAGAAACTCACTTGAAGGATTTTGTAT 2449
Qy 3786 GAGATTATGTCAGCAACAAAGCGCATGTCCTCCCACTCTGCAAGTTGCGGGGATG 3845
Db 2449 GAGATTATGTCAGCAACAAAGCGCATGTCCTCCCACTCTGCAAGTTGCGGGGATG 2499
Qy 3846 GATGCGGATTAAGCGGCTGCTGTTTCTGGAATCGACGATTTGCACTGCGGTAGAA 3905
Db 2499 GATGCGGATTAAGCGGCTGCTGTTTCTGGAATCGACGATTTGCACTGCGGTAGAA 2549
Qy 3906 CTCGCGAGGTCTGACGCTCAGGAGCAGCTGAACCACTGCGAGGGGATGAGCCC 3965
Db 2549 CTCGCGAGGTCTGACGCTCAGGAGCAGCTGAACCACTGCGAGGGGATGAGCCC 2605
Qy 3966 GGGGTGGGCAAGAACTCAGCATGAGATCCCGCGCTGGAAGATCATCAGCGGCGTC 4025
Db 2605 GGGGTGGGCAAGAACTCAGCATGAGATCCCGCGCTGGAAGATCATCAGCGGCGTC 2649
Qy 4026 CCGAAAAAGATCCGAAGCCCACTTTCATGAAGCGGCGGTGAATCGAAATCTCG 4085
Db 2649 CCGAAAAAGATCCGAAGCCCACTTTCATGAAGCGGCGGTGAATCGAAATCTCG 2705
Qy 4086 TGAATGAGGTGGGCGTCTGTTGTCGATTCATTGCAACCCAGAGTCCCGCTCAGAG 4145
Db 2705 TGAATGAGGTGGGCGTCTGTTGTCGATTCATTGCAACCCAGAGTCCCGCTCAGAG 2759
Qy 4146 AACTGTCAGAAAGCGATGAAGAGCGATGCGTGGAAAGCGGAGCGGATPCCGTAA 4205
Db 2759 AACTGTCAGAAAGCGATGAAGAGCGATGCGTGGAAAGCGGAGCGGATPCCGTAA 2819
Qy 4206 AGCAGAGAAAGGCTGACCCCATTCGCGCAAGCTCTTCAACCAATATCAAGGATGACC 4265
Db 2819 AGCAGAGAAAGGCTGACCCCATTCGCGCAAGCTCTTCAACCAATATCAAGGATGACC 2875

D	b	1592	GCTGCATTATGAATTCGGCCAAACGCGGGGAGAGCGGTTTGGCTATTTGGGCGCTCTTC	1651
Q	y	2946	CGCTTCCTCGCTCACTGACTGCTGCGCTCGGTGCTTCGCTGCGGCGAGCGATACAGC	3005
D	b	1652	CGTTCCTCGCTCACTGACTGCTGCGCTCGGTGCTTCGCTGCGGCGAGCGATACAGC	1711
Q	y	3006	TCACTCAAAGCGGTAATACGGTTATCCAGAGAAATCAGGGGATATACCGAGAAAGAAAT	3065
D	b	1712	TCACTCAAAGCGGTAATACGGTTATCCAGAGAAATCAGGGGATATACCGAGAAAGAAAT	1771
Q	y	3066	GTGAGCAAAAGCGCAGCAAAAGGCGCAGGAAACCGTAAAAAGGCGCGCTTGCTGCGCTTTT	3125
D	b	1772	GTGAGCAAAAGCGCAGCAAAAGGCGCAGGAAACCGTAAAAAGGCGCGCTTGCTGCGCTTTT	1831
Q	y	3126	CCATATGGCTCCGCCCCCTCTGACAGAGCATCAAAAAATGACAGCTCAAGTAGAGTGGCG	3185
D	b	1832	CCATATGGCTCCGCCCCCTCTGACAGAGCATCAAAAAATGACAGCTCAAGTAGAGTGGCG	1891
Q	y	3186	AAACCCGACAGACCTATTAAGATACAGAGCGTTTCCCTCGAAGCTCCCTCGTGCCTC	3245
D	b	1892	AAACCCGACAGACCTATTAAGATACAGAGCGTTTCCCTCGAAGCTCCCTCGTGCCTC	1951
Q	y	3246	TCCTGTTCCGACCCCTGCGCTTACCCGATACCTGTCCGCTTTCTCCCTTCGGAAAGCT	3305
D	b	1952	TCCTGTTCCGACCCCTGCGCTTACCCGATACCTGTCCGCTTTCTCCCTTCGGAAAGCT	2011
Q	y	3306	GGCGCTTTCTCATATGCTCAGCGCTGATAGGTAATCTCAGTTCCGATGAGGTCGTTCCGCTCCA	3365
D	b	2012	GGCGCTTTCTCATATGCTCAGCGCTGATAGGTAATCTCAGTTCCGATGAGGTCGTTCCGCTCCA	2071
Q	y	3366	GCTGCGCTGTGTGACGAAACCCCGCTTCAGCCCGACCGCTGCGCGCTTATCCGGTAACTA	3425
D	b	2072	GCTGCGCTGTGTGACGAAACCCCGCTTCAGCCCGACCGCTGCGCGCTTATCCGGTAACTA	2131
Q	y	3426	TCGCTTTGAGTCCAAACCCGGTAAACACAGATTTATCCGACTTGGCAGAGGCACTGGTAA	3485
D	b	2132	TCGCTTTGAGTCCAAACCCGGTAAACACAGATTTATCCGACTTGGCAGAGGCACTGGTAA	2191
Q	y	3486	CAGATTATGACAGAGCGAGTATGTATAGCGGTCTACAGAGTCTTGAAGTGTGGGCTTAA	3545
D	b	2192	CAGATTATGACAGAGCGAGTATGTATAGCGGTCTACAGAGTCTTGAAGTGTGGGCTTAA	2251
Q	y	3546	CTACGGCTACACTATGAGAGACATATTTGGTATCTGCGCTCTGCTGAAAGCACTTACCTT	3605
D	b	2252	CTACGGCTACACTATGAGAGACATATTTGGTATCTGCGCTCTGCTGAAAGCACTTACCTT	2311
Q	y	3606	CGGAAAAAGATGGGTAGCTCTGATTCGGGAAAACAACCAACCGCTGGTACCGGAGGTTT	3665
D	b	2312	CGGAAAAAGATGGGTAGCTCTGATTCGGGAAAACAACCAACCGCTGGTACCGGAGGTTT	2371
Q	y	3666	TTTTGTTTGCAAGCAGCAGATTTACGCGCAGAAAAAAAGATCTCAAGAAATCTCTTGTAT	3725
D	b	2372	TTTTGTTTGCAAGCAGCAGATTTACGCGCAGAAAAAAAGATCTCAAGAAATCTCTTGTAT	2431
Q	y	3726	CTTTCTTACGGGGTCTGACGCTCAGTGGAAAGAAACTCAGTTAAGGATTTTGGTCAT	3785
D	b	2432	CTTTCTTACGGGGTCTGACGCTCAGTGGAAAGAAACTCAGTTAAGGATTTTGGTCAT	2449
Q	y	3786	GAGATTATCGTGCACCAAAAGCGCCATCGCTCCCACTCTGACAGTTCCGGGGCATG	3845
D	b	2450	GAGATTATCGTGCACCAAAAGCGCCATCGCTCCCACTCTGACAGTTCCGGGGCATG	2449
Q	y	3846	GATGCGCGGATATGCGCGCTGTGCTTTCCTGGATCCGACCGATTTTGCACTGCGGTAAGA	3905
D	b	2450	GATGCGCGGATATGCGCGCTGTGCTTTCCTGGATCCGACCGATTTTGCACTGCGGTAAGA	2449
Q	y	3906	CTCCGCGAGTGTCCAGGCTCAGGCGAGGAGCTGAACCACTCCGGAAGGATCGAGGCC	3965
D	b	2450	CTCCGCGAGTGTCCAGGCTCAGGCGAGGAGCTGAACCACTCCGGAAGGATCGAGGCC	2449
Q	y	3966	GGGGTGGCGAAGAACTCCAGCATGATATCCCGCGCTGGAGGATCATCAGCCGCGCTC	4025
D	b	2450	GGGGTGGCGAAGAACTCCAGCATGATATCCCGCGCTGGAGGATCATCAGCCGCGCTC	2449

QY	4026	CCGGA AAAACGATTCCGAACCCCAACCTTTCA TAGAAGCGCGGTGGAATCGAAATCTCG	4085
Db	2450	-----	2449
QY	4086	TGATGACAGGTGTGGCGTCGCTTGTCGATCTTTCGAACCCAGAGTCCCGCTCAGAA G	4145
Db	2450	-----	CGCTCAGAG 2459
QY	4146	AACCTGTCAGAAAGCGCATAGAAAGCGCATGCGCTGCCAATCGGGAGCGGCATCCGTAA	4205
Db	2460	AACCTGTCAGAAAGCGCATAGAAAGCGCATGCGCTGCCAATCGGGAGCGGCATCCGTAA	2519
QY	4206	AGCAGCGAAGAAAGGGGTGAGCCCATTTGCGCGCAGAGCTCTTCAGCAATATCAGGGTAGCC	4265
Db	2520	AGCAGCGAAGAAAGGGGTGAGCCCATTTGCGCGCAGAGCTCTTCAGCAATATCAGGGTAGCC	2579
QY	4266	AACGCTATGTCCTTGATAGCGGTCCGCCAACCCAGCGCGCCACAGTCGATGAATCCAGAA	4325
Db	2580	AACGCTATGTCCTTGATAGCGGTCCGCCAACCCAGCGCGCCACAGTCGATGAATCCAGAA	2639
QY	4336	AAGCGGCATTTTTCACCATGATATTTGGGCAAGACAGGCATGCGATGGTCAACAGACGA	4385
Db	2640	AAGCGGCATTTTTCACCATGATATTTGGGCAAGACAGGCATGCGATGGTCAACAGACGA	2699
QY	4386	TCCTGCGCGTGGGCATGCGCGCTTGAGCCTTGCGAGCAAGTTCGCGTGGCGCAGCCCC	4445
Db	2700	TCCTGCGCGTGGGCATGCGCGCTTGAGCCTTGCGAGCAAGTTCGCGTGGCGCAGCCCC	2759
QY	4446	TGATGCTCTTGTGTCAGATCATCTCTGATCCAGACAGCGGCTTTCATCCAGATACGTCT	4505
Db	2760	TGATGCTCTTGTGTCAGATCATCTCTGATCCAGACAGCGGCTTTCATCCAGATACGTCT	2819
QY	4506	CGCTCGATGCGATGTTTGGCTTGGTGGTCGAATGGGACAGGTAGCGGATCAAGGTATGC	4565
Db	2820	CGCTCGATGCGATGTTTGGCTTGGTGGTCGAATGGGACAGGTAGCGGATCAAGGTATGC	2879
QY	4566	AGCGCGCGCATTTGATCAAGCCATGATGATATCTTTCGCGAGACAGCATGATGATGAC	4625
Db	2880	AGCGCGCGCATTTGATCAAGCCATGATGATATCTTTCGCGAGACAGCATGATGATGAC	2939
QY	4626	AGGAGATCTCTGCCCCCGGACCTTCCGCCAATAGACAGCAGTCCCTTCCGCTTCAGTACA	4685
Db	2940	AGGAGATCTCTGCCCCCGGACCTTCCGCCAATAGACAGCAGTCCCTTCCGCTTCAGTACA	2999
QY	4686	ACGTCGAGCAAGAGTGCAGCAAGAAAGCGCCGTGTGGCAGCCAGATAGCGCGCTGCC	4745
Db	3000	ACGTCGAGCAAGAGTGCAGCAAGAAAGCGCCGTGTGGCAGCCAGATAGCGCGCTGCC	3059
QY	4746	TCGTCTGTCGAGTTCAATCAAGGCACCCGACAGGTGCGTCTTGACAAAAGAACCGGGGCG	4805
Db	3060	TCGTCTGTCGAGTTCAATCAAGGCACCCGACAGGTGCGTCTTGACAAAAGAACCGGGGCG	3119
QY	4806	CCCTGCGCTGACAGCGCGAACAAGCGGCGCATCAAGACAGCCGATGTGTGTTGTGCCAG	4865
Db	3120	CCCTGCGCTGACAGCGCGAACAAGCGGCGCATCAAGACAGCCGATGTGTGTTGTGCCAG	3179
QY	4866	TCATAGCGGAATAGCTTCTCCACCCAGAGCGGCGGAGAACTTGGGTGCAATCATCTTGT	4922
Db	3180	TCATAGCGGAATAGCTTCTCCACCCAGAGCGGCGGAGAACTTGGGTGCAATCATCTTGT	3239
QY	4926	TCATTCAGACGAAACGATTCCTATCTCTGTCTTGATTCAGATCTTGATCCCTGGCGCAT	4988
Db	3240	TCATTCAGACGAAACGATTCCTATCTCTGTCTTGATTCAGATCTTGATCCCTGGCGCAT	3299
QY	4986	CAGATCTCTGGCGGCAAGAAAGCATCAGATTATCTTTCAGAGGCTTCCCAACTTACCA	5045
Db	3300	CAGATCTCTGGCGGCAAGAAAGCATCAGATTATCTTTCAGAGGCTTCCCAACTTACCA	3355
QY	5046	GAGGGCGCCCAAGCTGGCAATTCGGGTTCGCTGTGTCATAAACCGCCCAAGTATGC	5105
Db	3360	GAGGGCGCCCAAGCTGGCAATTCGGGTTCGCTGTGTCATAAACCGCCCAAGTATGC	3415

Qy 5106 TATGCCATGTAAAGCCACTGCAAGCTACCTGCTTCTT 5146
Db 3420 AACTGTGGAAAGGCGATCGGTGGCGGCTTCTGCTATT 3460

RESULT 10
US-10-764-818A-29
; Sequence 29, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUT
; TITLE OF INVENTION: HERD ANIMALS
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10764.818A
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; OTHER INFORMATION: Codon optimized plasmid for GHRH expression.
US-10-764-818A-29

Query Match 30.4%; Score 1603.8; DB 11; Length 3534;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

Qy 2706 CTAGACGTAATCATGTCATAGCTGTTCTGTGTAATTTGTTATCCGCTCACAATTC 2765
Db 1412 CTGGCGTAATCATGTCATAGCTGTTCTGTGTAATTTGTTATCCGCTCACAATTC 1471
Qy 2766 ACAACAATACAGACCGGAGACATTAAGTTAAAGCTGGGCTCTAATAGTAGCTA 2825
Db 1472 ACAACAATACAGACCGGAGACATTAAGTTAAAGCTGGGCTCTAATAGTAGCTA 1531
Qy 2826 ACTCACATTAATGCTGTGCGCTACCTGCGGCTTCCAGTCGGGAAACCTGTGTCGA 2885
Db 1532 ACTCACATTAATGCTGTGCGCTACCTGCGGCTTCCAGTCGGGAAACCTGTGTCGA 1591
Qy 2886 GCTGCATTAATGAATCGGCCAACCGCGGGAGAGAGCGGTTTGCGATTGCGGCTCTTC 2945
Db 1592 GCTGCATTAATGAATCGGCCAACCGCGGGAGAGAGCGGTTTGCGATTGCGGCTCTTC 1651
Qy 2946 CGCTTCTCGCTCACTGACTGCTGCGCTCGCTGCTTTCGCTGCGCGAGCGGTATCAGC 3005
Db 1652 CGCTTCTCGCTCACTGACTGCTGCGCTCGCTGCTTTCGCTGCGCGAGCGGTATCAGC 1711
Qy 3006 TCACTCAAGGCGGTATAGCGTTATCAAGATCAAGAGGATTAACGCAAGAAAGCAT 3065
Db 1712 TCACTCAAGGCGGTATAGCGTTATCAAGATCAAGAGGATTAACGCAAGAAAGCAT 1771
Qy 3066 GTGAGCAAAAGGCGCAGCAAAAGGCGCAGAAACCTTAAGAAAGCGCTTGCTGCGGTTTT 3125
Db 1772 GTGAGCAAAAGGCGCAGCAAAAGGCGCAGAAACCTTAAGAAAGCGCTTGCTGCGGTTTT 1831
Qy 3126 CCAATAGCTCGGCGCCCTCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGTGCGG 3185
Db 1832 CCAATAGCTCGGCGCCCTCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGTGCGG 1891
Qy 3186 AAACCCGACAGGATTAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGGCGCTC 3245
Db 1892 AAACCCGACAGGATTAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGGCGCTC 1951
Qy 3246 TCTGTTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGAAGCGT 3305
Db 1952 TCTGTTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGAAGCGT 2011
Qy 3306 GGGCGCTTTCATAGCTACGCTGTAGGTATCTCAGTTGGGTGAGTCTTTCGCTCAA 3365
Db 2012 GGGCGCTTTCATAGCTACGCTGTAGGTATCTCAGTTGGGTGAGTCTTTCGCTCAA 2071

Qy 3366 GCTGGCGTGTGTGACGAAACCCCGTTACGCCGCGAGCGGCTTATCCGGTAATA 3425
Db 2072 GCTGGCGTGTGTGACGAAACCCCGTTACGCCGCGAGCGGCTTATCCGGTAATA 2131
Qy 3426 TCGTCTTGAAGTCAACCCCGGTAGACAGACTTATCCGCACTGGCAGCAGCCACTGTATA 3485
Db 2132 TCGTCTTGAAGTCAACCCCGGTAGACAGACTTATCCGCACTGGCAGCAGCACTGTATA 2191
Qy 3486 CAGATTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGAGTTCTTGAAGTGTGGCTTAA 3545
Db 2192 CAGATTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGAGTTCTTGAAGTGTGGCTTAA 2251
Qy 3546 CTAGGCGTACCTAGAAAGACAGATTGTGATGTGGCTGTGTAAGCCAGTTACTT 3605
Db 2252 CTAGGCGTACCTAGAAAGACAGATTGTGATGTGGCTGTGTAAGCCAGTTACTT 2311
Qy 3606 CGGAAAAAGATTGTAGCTCTTGATCCGCAAAACCAACCGCTGTAGCGGTGTTT 3665
Db 2312 CGGAAAAAGATTGTAGCTCTTGATCCGCAAAACCAACCGCTGTAGCGGTGTTT 2371
Qy 3666 TTTTGTTCAGACAGATTAACGCGCAGAAAAAGATCTCAAGAGATCCTTGAT 3725
Db 2372 TTTTGTTCAGACAGATTAACGCGCAGAAAAAGATCTCAAGAGATCCTTGAT 2431
Qy 3726 CTTTCTACGGGGCTGACCGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTGTGCAT 3785
Db 2432 CTTTCTACGGGGCTGACCGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTGTGCAT 2449
Qy 3786 GAGATTATCGTCCGACCAAGCGGCAATCGTGCTCCCACTCTCAGATTCCGGGGCATG 3845
Db 2450 GAGATTATCGTCCGACCAAGCGGCAATCGTGCTCCCACTCTCAGATTCCGGGGCATG 2449
Qy 3846 GATGCGGATAGCGCTGCTGTTCTTCTGATGCGAGCGAATTTGCACTGCCGTAGAA 3905
Db 2450 GATGCGGATAGCGCTGCTGTTCTTCTGATGCGAGCGAATTTGCACTGCCGTAGAA 2449
Qy 3906 CTCGCGAGGTCGTCCAGGCTCAGGCGACGCTGAAACCACTCGCGAGGGGATTCGAGCCC 3965
Db 2450 CTCGCGAGGTCGTCCAGGCTCAGGCGACGCTGAAACCACTCGCGAGGGGATTCGAGCCC 2449
Qy 3966 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGTGGAGATCATCCAGCGCGCTC 4025
Db 2450 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGTGGAGATCATCCAGCGCGCTC 2449
Qy 4026 CCGAAAAAGATTCCGAAGCCCAACTTTCATAGAAAGCGCGGTGGAATCGAAATCTCG 4085
Db 2450 CCGAAAAAGATTCCGAAGCCCAACTTTCATAGAAAGCGCGGTGGAATCGAAATCTCG 2449
Qy 4086 TGATGCGAGTTGGGCGCTCGCTTGTGCTGATTTGGAACCCAGAGTCCCGCTCAGAAAG 4145
Db 2450 TGATGCGAGTTGGGCGCTCGCTTGTGCTGATTTGGAACCCAGAGTCCCGCTCAGAAAG 2459
Qy 4146 AACTCGTCAAGAGGCGATTAAGAGCGATGCGTGCATTCGGAGCGCGGATACCGTTAA 4205
Db 2460 AACTCGTCAAGAGGCGATTAAGAGCGATGCGTGCATTCGGAGCGCGGATACCGTTAA 2519
Qy 4206 AGCAGAGAAAGCGGTCAAGCCCAATTCGCGCGCAAGCTTTTCAACAATATCAGCGTAAAGCC 4265
Db 2520 AGCAGAGAAAGCGGTCAAGCCCAATTCGCGCGCAAGCTTTTCAACAATATCAGCGTAAAGCC 2579
Qy 4266 AAGGCTATGTCGATAGCGGTCCGCAACCCAGCGGCGCAAGTTCGATGATTCAGAA 4325
Db 2580 AAGGCTATGTCGATAGCGGTCCGCAACCCAGCGGCGCAAGTTCGATGATTCAGAA 2639
Qy 4326 AAGCGCATTTTTCACATGATATTTCGCAACAGAGCATTCGCAATGGGTCAAGCAGAA 4385
Db 2640 AAGCGCATTTTTCACATGATATTTCGCAACAGAGCATTCGCAATGGGTCAAGCAGAA 2699
Qy 4386 TCTTCGCGGTGCGGCAATGCGCGCTTGAAGCTGCGCAACAGATTTCGCTGCGCGAGGCC 4445
Db 2700 TCTTCGCGGTGCGGCAATGCGCGCTTGAAGCTGCGCAACAGATTTCGCTGCGCGAGGCC 2759

Db 2450 ----- 2449
Qy 3846 GATGGCGGATAGCGCGTCTGTTTCTTGATGCCGACGATTTTGACTGCGGTAGAA 3905
Db 2450 ----- 2449
Qy 3906 CTCCGCGAGGTCTGTCAGAGCTCAGGACAGCTGAACCACTCGGAGGGATCGAGCC 3965
Db 2450 ----- 2449
Qy 3966 GGGGTGGCGAAGAACTTCAGCATGAGATCCCGGCTGAGAGATCATCAGCCGCGTC 4025
Db 2450 ----- 2449
Qy 4026 CCGGAAACGATTCGGAAGCCCACTTTCAATAGAGGCGGCGGTGAATCGAAATCTCG 4085
Db 2450 ----- 2449
Qy 4086 TGATGGCAGTGGGCGTGGCTGTGTCATTTCCAAACCCAGAGTCCCGCTCAGAA 4145
Db 2450 ----- 2459
Qy 4146 AACTGCTCAGAAAGCGCATAGAAAGCGATGCGCTGCGAATCGGAGCGCGATACCGTAA 4205
Db 2460 AACTGCTCAGAAAGCGCATAGAAAGCGATGCGCTGCGAATCGGAGCGCGATACCGTAA 2519
Qy 4206 AGCAGCGAAGCGGATGAGCCCATTTGCGCGGAGGCTTTGAGCAATATCAGGGTACC 4285
Db 2520 AGCAGCGAAGCGGATGAGCCCATTTGCGCGGAGGCTTTGAGCAATATCAGGGTACC 2579
Qy 4266 AACGCTATGCTCTGATAGCGGTCCGCAACCCAGCGCGGACAGTGCATGATCCAGAA 4325
Db 2580 AACGCTATGCTCTGATAGCGGTCCGCAACCCAGCGCGGACAGTGCATGATCCAGAA 2639
Qy 4326 AAGCGGCATTTTCCACATGATATTCGCGAAGAGGATGCGATGGGTACAGACGAGA 4385
Db 2640 AAGCGGCATTTTCCACATGATATTCGCGAAGAGGATGCGATGGGTACAGACGAGA 2699
Qy 4386 TCCCTGCGCGTCCGCGATGCGCGCTTGAGCCTGGCGAAACAGTTGGCTGGCGAGCC 4445
Db 2700 TCCCTGCGCGTCCGCGATGCGCGCTTGAGCCTGGCGAAACAGTTGGCTGGCGAGCC 2759
Qy 4446 TGATGCTCTTCTGTCAGATCATCTGATCGACAGAACCGGCTTCATCCGATCGTGCT 4505
Db 2760 TGATGCTCTTCTGTCAGATCATCTGATCGACAGAACCGGCTTCATCCGATCGTGCT 2819
Qy 4506 CGCTCGATGCGATGTTTGGTGGTTCGATGCGAGGAGGTAGCCGATCAAGCGTATGC 4565
Db 2820 CGCTCGATGCGATGTTTGGTGGTTCGATGCGAGGAGGTAGCCGATCAAGCGTATGC 2879
Qy 4566 AGCGCGCGCATTTGATCAAGCATATGATGATCTTTCTCGGAGAGACAGTGCATGAC 4625
Db 2880 AGCGCGCGCATTTGATCAAGCATATGATGATCTTTCTCGGAGAGACAGTGCATGAC 2939
Qy 4626 AGGAGATCTGCGCCCGGACCTTGCGCAATAGCAGCGACGTCCCTCCGCTTCAGTACA 4685
Db 2940 AGGAGATCTGCGCCCGGACCTTGCGCAATAGCAGCGACGTCCCTCCGCTTCAGTACA 2999
Qy 4686 ACCTCGAGCAGAGCTGGCGAAGAACCGCTGCTGCGACGACGATAGCCGCGCTGCC 4745
Db 3000 ACCTCGAGCAGAGCTGGCGAAGAACCGCTGCTGCGACGACGATAGCCGCGCTGCC 3059
Qy 4746 TCGTCTCTGCAAGTTATTCAGGGACCGGACAGGTCTGTTGACAAAAGAACCGGGCGC 4805
Db 3060 TCGTCTCTGCAAGTTATTCAGGGACCGGACAGGTCTGTTGACAAAAGAACCGGGCGC 3119
Qy 4806 CCTGCGCTGACAGCCGGAACAGCGCGCATCAGAGCAGCGATGATCTGTTGCGCCAG 4865
Db 3120 CCTGCGCTGACAGCCGGAACAGCGCGCATCAGAGCAGCGATGATCTGTTGCGCCAG 3179
Qy 4866 TCATAGCCGAATAGCTTCTCACCAGCGCGCGAGAACCTGCGTGCATTCATCTTGT 4925

Db 3180 TCATAGCCGAATAGCTTCTCACCAGCGCGAGAACCTGCGTGCATTCATCTTGT 3239
Qy 4926 TCATAGCCGAATAGCTTCTCACCAGCGCGAGAACCTGCGTGCATTCATCTTGT 4985
Db 3240 TCATAGCCGAATAGCTTCTCACCAGCGCGAGAACCTGCGTGCATTCATCTTGT 3299
Qy 4986 CAGATCCCTGGCGGAGAAAGCATCAGTTTACTTTGAGGAGCTTCCCAACCTTACA 5045
Db 3300 CAGATCCCTGGCGGAGAAAGCATCAGTTTACTTTGAGGAGCTTCCCAACCTTACA 3359
Qy 5046 GAGGCGCGCCAGCTGCGCAATTCGATTCGCTTGTCTGTCATTAACCGCCAGTAC 5105
Db 3360 GAGGCGCGCCAGCTGCGCAATTCGATTCGCTTGTCTGTCATTAACCGCCAGTAC 3419
Qy 5106 TATGCCATGTAAAGCCCACTGCAAGCTACTGCTTCTCTT 5146
Db 3420 AACTGTTGGAAAGGCGATGCGTGGGCGCTTCTGCTAAT 3460

RESULT 12
US-10-764-818A-26
; Sequence 26, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CULI
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10764,818A
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 3558
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence for the inducible pGR174 with human GHRH
US-10-764-818A-26

Query Match 30.4%; Score 1603.4; DB 11; Length 3558;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2021; Conservative 1; Mismatches 27; Indels 392; Gaps 1;

Qy 2706 CTGAGCTATCATGCTCATAGCTGTTTCTGTTGTAATTTTATCCGCTCACATTTCC 2765
Db 1253 CTGAGCTATCATGCTCATAGCTGTTTCTGTTGTAATTTTATCCGCTCACATTTCC 1312
Qy 2766 ACAACAATATGAGCGCGAAGCATTAAGTAAAGCTGGGGTGCCTTAATGAGTACCTA 2825
Db 1313 ACAACAATATGAGCGCGAAGCATTAAGTAAAGCTGGGGTGCCTTAATGAGTACCTA 1372
Qy 2826 ACTCAATTAATGCGTTGCGTCACTGCGCGCTTTCAGTCCGGAACCTGTCGTGCA 2885
Db 1373 ACTCAATTAATGCGTTGCGTCACTGCGCGCTTTCAGTCCGGAACCTGTCGTGCA 1432
Qy 2886 GCTGCATTAATGATGCGCCCAACCGCGGGAAGGCGTTTGGCTTAATGGGCGCTTTC 2945
Db 1433 GCTGCATTAATGATGCGCCCAACCGCGGGAAGGCGTTTGGCTTAATGGGCGCTTTC 1492
Qy 2946 CGCTTCCTGCTCACTGAGCTGCGTGGCGTGGCTGCTTCCGCTGCGGAGCGGATACGC 3005
Db 1493 CGCTTCCTGCTCACTGAGCTGCGTGGCGTGGCTGCTTCCGCTGCGGAGCGGATACGC 1552
Qy 3006 TCACTCAAAAGCGGTATACGTTATCCACAGATCAGGGGATTAACGACGAAAGAACAT 3065
Db 1553 TCACTCAAAAGCGGTATACGTTATCCACAGATCAGGGGATTAACGACGAAAGAACAT 1612
Qy 3066 GTAGCAAAAAGGCGACGAAAGCGGAAACCTTAATAAGGCGCGTGTGCGCTTTT 3125
Db 1613 GTAGCAAAAAGGCGACGAAAGCGGAAACCTTAATAAGGCGCGTGTGCGCTTTT 1672
Qy 3126 CATAGGCTTCCGCGCCCTGACGAGCATCAAAAATTCAGCGCTCAAGTCAAGGTGGCG 3185

|||||
Db 1673 CCAATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCG 1732
Qy 3186 AAACCCGACGAGACTATAAAGATACCGAGGGTTTCCCCCGGAAGCTCCCTCGTGGGCTC 3245
Db 1733 AAACCCGACGAGACTATAAAGATACCGAGGGTTTCCCCCGGAAGCTCCCTCGTGGGCTC 1792
Qy 3246 TCTGTTCCGACCCCTGCGGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAACGT 3305
Db 1793 TCTGTTCCGACCCCTGCGGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAACGT 1852
Qy 3306 GGGCGCTTTCTCATAGCTCAGGCTGTAGTATCTCAATTCGCTGATAGGTGCTTCCCA 3365
Db 1853 GGGCGCTTTCTCATAGCTCAGGCTGTAGTATCTCAATTCGCTGATAGGTGCTTCCCA 1912
Qy 3366 GCTGGGCTGTGTGACGAAACCCCGCTTACGCGCCGACCGGCTGCGCTTATCCGGTACTA 3425
Db 1913 GCTGGGCTGTGTGACGAAACCCCGCTTACGCGCCGACCGGCTGCGCTTATCCGGTACTA 1972
Qy 3426 TCGTCTTGAAGTCGAACCCCGGTAAACA GACTTATCGCCACTGCGACAGCCACTGTGTA 3485
Db 1973 TCGTCTTGAAGTCGAACCCCGGTAAACA GACTTATCGCCACTGCGACAGCCACTGTGTA 2032
Qy 3486 CAGGATTAAGCAGACCGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGTGGCTTAA 3545
Db 2033 CAGGATTAAGCAGACCGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGTGGCTTAA 2092
Qy 3546 CTAAGGCTCACTAGAAAGAACATATTGTGATCTGCGCTCTGCTGAAGCCAGTTTACTT 3605
Db 2093 CTAAGGCTCACTAGAAAGAACATATTGTGATCTGCGCTCTGCTGAAGCCAGTTTACTT 2152
Qy 3606 CGGAAAAAGATTGGTATCTTGAATCCGGCAAA CAAACACCGCTGTGTAGCGGTGTT 3665
Db 2153 CGGAAAAAGATTGGTATCTTGAATCCGGCAAA CAAACACCGCTGTGTAGCGGTGTT 2212
Qy 3666 TTTTGTGTGCAAGACGAGTTAAGCGCGCAAAAAAGATCTCAAGAGATCTTTGAT 3725
Db 2213 TTTTGTGTGCAAGACGAGTTAAGCGCGCAAAAAAGATCTCAAGAGATCTTTGAT 2272
Qy 3726 CTTTCTTCAAGGCGGTCTGACGCTCAGTGTGAAGAAAACTCAGTTAAGGGATTTTGTCTAT 3785
Db 2273 CTTTCTTCAAGGCGGTCTGACGCTCAGTGTGAAGAAAACTCAGTTAAGGGATTTTGTCTAT 2290
Qy 3786 GAGATTATCTGACCAAGCGGCGCATGTGCTCCCACTCTGCAAGTTCCGGGGCATG 3845
Db 2291 ----- 2290
Qy 3846 GATGCGCGATAGCCGCTGTGTTTCTGTAGTCCGACGATTGTGCACTGCGGTAGAA 3905
Db 2291 ----- 2290
Qy 3906 CTCGCGAGGTCTGTCAGCCTCAGCGACAGCTGAACCACTCGCGAGGGATCGAGCCC 3965
Db 2291 ----- 2290
Qy 3966 GGGGTGGCGAAGACTCCAGATGAGATCCCGCGGTGAGAGATCATCGACGGGCTC 4025
Db 2291 ----- 2290
Qy 4026 CCGAAAAAGATTCCGAAGCCCACTTTTCATAGAGCGCGGTGAGTGAATCGAATCTCG 4085
Db 2291 ----- 2290
Qy 4086 TGATGCGAGGTTGGCGCTGCTTGGTCAATTTTCGAACCCGAGATCCCGCTCAGAG 4145
Db 2291 ----- 2300
Qy 4146 AACTGTCAGAAAGCGATAGAAAGCGATGCGTCGATCGGAGCGCGCATACCGTAA 4205
Db 2301 AACTGTCAGAAAGCGATAGAAAGCGATGCGTCGATCGGAGCGCGCATACCGTAA 2360
Qy 4206 AGCAGAGAGAGCGGTCAAGCCCATTCGCGCAAGCTTTCAGCAATATCAAGGTAGCC 4265
|||||

Db 2361 AGCAGAGAGAGCGGTCAAGCCCATTCGCGCAAGCTTTCAGCAATATCAAGGTAGCC 2420
Qy 4266 AAGCTATGCTCTGATATACCGGTTCGCCACACCAAGCCGCCACAGTGTGAATTCAGAA 4325
Db 2421 AAGCTATGCTCTGATATACCGGTTCGCCACACCAAGCCGCCACAGTGTGAATTCAGAA 2480
Qy 4326 AAGCGCCATTTTCCACATATATTTCCGGAAGAGAGAGATGCCATGGGTTCACGACGGA 4385
Db 2481 AAGCGCCATTTTCCACATATATTTCCGGAAGAGAGAGATGCCATGGGTTCACGACGGA 2540
Qy 4386 TCCCTGCGGTGGGGATGCGCGCTTGAAGCTGCGGAACAGTTGCGTGGCGAGCCC 4445
Db 2541 TCCCTGCGGTGGGGATGCGCGCTTGAAGCTGCGGAACAGTTGCGTGGCGAGCCC 2600
Qy 4446 TGATGCTCTTGTCCAGATCATCTGATTCAGACAGACCGGCTTCCATCCGATAGTCT 4505
Db 2601 TGATGCTCTTGTCCAGATCATCTGATTCAGACAGACCGGCTTCCATCCGATAGTCT 2660
Qy 4506 CGCTGATGCGGATGTTTGGCTTGTGTGATGATGAGGAGGTAGCCGATCAAGCGTATGC 4565
Db 2661 CGCTGATGCGGATGTTTGGCTTGTGTGATGATGAGGAGGTAGCCGATCAAGCGTATGC 2720
Qy 4566 AGCCGCGCATTCATTCAGCCATGATGATATCTTCTCGGACAGAGAGAGGTAGATAC 4625
Db 2721 AGCCGCGCATTCATTCAGCCATGATGATATCTTCTCGGACAGAGAGAGGTAGATAC 2780
Qy 4626 AGGAGATCTGCCCCCGGCACTTCCGCCAATATAGCAACAGTCCCTCCGCTTCAAGTGA 4685
Db 2781 AGGAGATCTGCCCCCGGCACTTCCGCCAATATAGCAACAGTCCCTCCGCTTCAAGTGA 2840
Qy 4686 AGCTGAGACAGCTGCGCAAGAAAGCCCGTGTGTGCGACGACAGATAGCCGCTGCG 4745
Db 2841 AGCTGAGACAGCTGCGCAAGAAAGCCCGTGTGTGCGACGACAGATAGCCGCTGCG 2900
Qy 4746 TCGTCTGAGTTCAATTCAGGACACCGGACAGGTGCTTGTGAACAAAAAGAACCGGGGCG 4805
Db 2901 TCGTCTGAGTTCAATTCAGGACACCGGACAGGTGCTTGTGAACAAAAAGAACCGGGGCG 2960
Qy 4806 CCTGTGCGACAGCCCGGAACCGGGGATCAGAGACAGCCATGTCTGTGTGCCAG 4865
Db 2961 CCTGTGCGACAGCCCGGAACCGGGGATCAGAGACAGCCATGTCTGTGTGCCAG 3020
Qy 4866 TCATAGCCGAATAGCTCTTCACCCCAAGCGGCGGAGAACCTGTGCAATCATCTTGT 4925
Db 3021 TCATAGCCGAATAGCTCTTCACCCCAAGCGGCGGAGAACCTGTGCAATCATCTTGT 3080
Qy 4926 TCAATCATGGAAGCATCTCTATCTGTCTTGTATCAGATCTTGAATCCCTGGCCAT 4985
Db 3081 TCAATCATGGAAGCATCTCTATCTGTCTTGTATCAGATCTTGAATCCCTGGCCAT 3140
Qy 4986 CAGATCTTGGGCGGCAAGAAAGCATCCAGTTTATCTTTCAGAGGCTTCCCACTTACCA 5045
Db 3141 CAGATCTTGGGCGGCAAGAAAGCATCCAGTTTATCTTTCAGAGGCTTCCCACTTACCA 3200
Qy 5046 GAGGGGCGCCCAAGCTTGGCAATTCGGTTGCTTGTCTTCATPAAAACCGCCAGTCTAGC 5105
Db 3201 GAGGGGCGCCCAAGCTTGGCAATTCGGTTGCTTGTCTTCATPAAAACCGCCAGTCTAGC 3260
Qy 5106 TATGCGCATGTAGCCCATCTGCAAGCTACTGTCTTCTCT 5146
Db 3261 TATGCGCATGTAGCCCATCTGCAAGCTACTGTCTTCTCT 3301
|||||

RESULT 13
US-11-194-143-27
; Sequence 27, Application US/11194143
; Publication No. US20060068496A1
; GENERAL INFORMATION:
; APPLICANT: James H. Kelly
; TITLE OF INVENTION: Differentiation of Stem Cells
; FILE REFERENCE: 16016.000702
; CURRENT APPLICATION NUMBER: US/11/194,143
; CURRENT FILING DATE: 2005-07-29

Db 7729 CGCTTGCATTTATTCAGGCGACCGGACGGTCCGCTTGAACAAAAGAACCGGCGCC 7788
Qy 4807 CCGCGCTGACAGCCGGGACACGCGGCATCAGAGAGCCGATTGTCGTGGCCAGT 4866
Db 7789 CCGCGCTGACAGCCGGGACACGCGGCATCAGAGAGCCGATTGTCGTGGCCAGT 7848
Qy 4867 CATAGCCGAATGACCTCTCCACCCGAGCGCGGAGAACTCGTGCATTCATCTTGT 4926
Db 7849 CATAGCCGAATGACCTCTCCACCCGAGCGCGGAGAACTCGTGCATTCATCTTGT 7908
Qy 4927 CAATTCATGGAAGAAAGATCCATCCCTGCTCTTGATCAGATCTTG 4971
Db 7909 CAATTCATGGAAGAAAGATCCATCCCTGCTCTTGATCAGATCTTIG 7953

RESULT 14

US-11-005-216-4/c
; Sequence 4, Application US/11005216
; Publication No. US20050287633A1
; GENERAL INFORMATION:
; APPLICANT: McIntyre, Peter
; APPLICANT: James, Iain Frazer
; TITLE OF INVENTION: Human Vanilloid Receptor
; FILE REFERENCE: 4-30875A
; CURRENT APPLICATION NUMBER: US/11/005,216
; PRIOR FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US/09/533,220
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 1.30
; SEQ ID NO 4
; LENGTH: 4886
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-005-216-4

Query Match 29.7%; Score 1570; DB 17; Length 4886;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

Qy 3008 ACTCAAGGCGGTATATGCGTTATCCACAGATCAGGCGGATTAACGAGAAAGACATGT 3067
Db 4295 AATCAATGCGGATATACGGTTATCCAGATACAGGAGATTAACGAGAAAGACATGT 4236
Qy 3068 GAGCAAAAGGCGACAAAGGCGCAGAACCGTAAAAAAGCGCGCTTCTGGCGTTTTC 3127
Db 4235 GAGCAAAAGGCGACAAAGGCGCAGAACCGTAAAAAAGCGCGCTTCTGGCGTTTTC 4176
Qy 3128 ATAGAGCTCCGCGCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGTGGCGAA 3187
Db 4175 ATAGAGCTCCGCGCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGTGGCGAA 4116
Qy 3188 ACCGCAAGAGCTTAAGATACAGAGGTTCCCGCTGAAGTCCCTCGTGCGCTCTC 3247
Db 4115 ACCGCAAGAGCTTAAGATACAGAGGTTCCCGCTGAAGTCCCTCGTGCGCTCTC 4056
Qy 3248 CTGTTCCGACCCCTGCGTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAAGCGTG 3307
Db 4055 CTGTTCCGACCCCTGCGTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAAGCGTG 3296
Qy 3308 CGCTTTCTCATAGCTCAGCGCTGATGATCTCAAGTGGGTAGTGGTCTGCTCAAGC 3367
Db 3395 CGCTTTCTCATAGCTCAGCGCTGATGATCTCAAGTGGGTAGTGGTCTGCTCAAGC 3396
Qy 3368 TGCGCTGATGAGAAAGGCGCGCTTACCGCGAGCGCGTGCCTTATCCGTAATCTATC 3427
Db 3335 TGCGCTGATGAGAAAGGCGCGCTTACCGCGAGCGCGTGCCTTATCCGTAATCTATC 3376
Qy 3428 GTCTTGAATCCAAACCGGTAAGACAGATTAATGCGCATGCGCAGACGCACTGTAACA 3487

Db 3875 GTCTTGAATCCAAACCGGTAAGACAGATTAATGCGCATGCGCAGACGCACTGTAACA 3816
Qy 3488 GGATTTAGCAAGCGAGATATGTAAGCGGTGCTACAGAGTTCTTTAAAGTGGTGAATCT 3547
Db 3815 GGATTTAGCAAGCGAGATATGTAAGCGGTGCTACAGAGTTCTTTAAAGTGGTGAATCT 3756
Qy 3548 AGGCTACACATGAAGAAAGATTTGATATGCGCTCTGCGAGCGAGTAACTCTTCG 3607
Db 3755 AGGCTACACATGAAGAAAGATTTGATATGCGCTCTGCGAGCGAGTAACTCTTCG 3696
Qy 3608 GAAAAAGATTGGTATGCTCTTATCCGCAACAAACACCGCTGTAAGCGGTGTTTTT 3667
Db 3695 GAAAAAGATTGGTATGCTCTTATCCGCAACAAACACCGCTGTAAGCGGTGTTTTT 3636
Qy 3668 TTGTTTGCAGACAGATTAAGCGCAAAAAAGATTTCAAGATCTTGTGATCT 3727
Db 3635 TTGTTTGCAGACAGATTAAGCGCAAAAAAGATTTCAAGATCTTGTGATCT 3576
Qy 3728 TTTTCAAGGAGTCTGACGCTCAGTGAAGAAAGAACTCAGCTTAAGGATTTTGTATGA 3787
Db 3575 TTTTCAAGGAGTCTGACGCTCAGTGAAGAAAGAACTCAGCTTAAGGATTTTGTATGA 3516
Qy 3788 GATTAATGTCGACCAAGCGGCTATGCTCTTAAATTAAGATTTTAATCA 3819
Db 3515 GATTAATCAAAAGATCTTCACTAGATCTTTTAAATTAAGATTTTAATCA 3456
Qy 3820 -----CCCACTCCGAGTTCGGG 3840
Db 3455 TCTAAAGTATATATGATGATACCTGAGGCTATGCGAGGCTGCGCCCGAGCTTGGCTG 3396
Qy 3841 GCATGATGCGCGGATGACGCGTCTGCTGTTCTGATGCGCAGCGATTTGACGCGG 3900
Db 3395 CGAGCCCTGCGCTTCAACCGAACTTGGGGGTGGGGGAAAAAGAAAGCGCGG 3336
Qy 3901 -----TAGAATCCGCGAGTCTGCTCAAGCTCAGGACGACGCTGAACCAAC 3946
Db 3335 CGTATTGCGCCCAATGAGGCTCTCGGTGGGTATTCAGAGTGCAGCGCTGGACGAA 3276
Qy 3947 TCGCGAGGGGATCGA----- 3961
Db 3275 CCGCGGTTTATGAAACAAACGACCCAGACCGGTATTTATCTGTCTTTTATTTGCGG 3216
Qy 3962 -----GCCCG 3967
Db 3215 TCATAGCGGAGTCTTCGATATGTCCTTCCGTGTTCAATTAACCTCCCTAG 3156
Qy 3968 GGTGGCGGAAAGATCTCAGATGAGATCCCCCGCTGAGATCATCCAGCGCGGTCCC 4027
Db 3155 GGTGGCGGAAAGATCTCAGATGAGATCCCCCGCTGAGATCATCCAGCGCGGTCCC 3096
Qy 4028 GGAAGAGATTCGAGAGCCCAACCTTCAATGAGAGCGCGGTGAATGAATCTCTGT 4087
Db 3095 GGAAGAGATTCGAGAGCCCAACCTTCAATGAGAGCGCGGTGAATGAATCTCTGT 3036
Qy 4088 ATGCGAGTTGGCGTCTGCTGCTGATTTGAACTCCAGAGTCCGCTGAGAGAA 4147
Db 3035 ATGCGAGTTGGCGTCTGCTGCTGATTTGAACTCCAGAGTCCGCTGAGAGAA 2976
Qy 4148 CTGCTCAAGAGCGATTAAGAGCGATGCGCTGCGAATGGGAGCGGCGATCCGTAAG 4207
Db 2975 CTGCTCAAGAGCGATTAAGAGCGATGCGCTGCGAATGGGAGCGGCGATCCGTAAG 2916
Qy 4208 CACGAGAAAGCGGTACGCTTCCGCGCAAGCTTTCAGCAATATCAAGGTAAGCCAA 4267
Db 2915 CACGAGAAAGCGGTACGCTTCCGCGCAAGCTTTCAGCAATATCAAGGTAAGCCAA 2856
Qy 4268 CGCTATGCTCTGATGAGCGGTCCGCAACCCAGCGCGCAAGTGCATGATATCAAGAAA 4327
Db 2855 CGCTATGCTCTGATGAGCGGTCCGCAACCCAGCGCGCAAGTGCATGATATCAAGAAA 2796
Qy 4328 GCGGCAATTTTCAACATATTTGCGCAAGAGGATGCGCATGGGTCAACGAGATC 4387
Db 2795 GCGGCAATTTTCAACATATTTGCGCAAGAGGATGCGCATGGGTCAACGAGATC 2736

QY 4388 CTCGCCCTGCGGATGCGCGCTTGAAGCTGCGGAAACAGTTCGGCTGCGCGAGCCCTTG 4447
DB 2735 CTCGCCCTGCGGATGCGCGCTTGAAGCTGCGGAAACAGTTCGGCTGCGCGAGCCCTTG 2676
QY 4448 ATGCTCTTGTGCAATCATCTCTGATCGCAAGACCGGCTTCATTCGAGTACGTGCTG 4507
DB 2675 ATGCTCTTGTGCAATCATCTCTGATCGCAAGACCGGCTTCATTCGAGTACGTGCTG 2616
QY 4508 CTCGATGCGATGTTTCGCTTGGTGGTGAATGGGGAGGTAGCGGATCAAGGGTATGCA 4567
DB 2615 CTCGATGCGATGTTTCGCTTGGTGGTGAATGGGGAGGTAGCGGATCAAGGGTATGCA 2556
QY 4558 CCGCGCGATTTGATCAGCCATGATGATACTTCTCGGAGAGAGCAAGGTGATGACAG 4627
DB 2555 CCGCGCGATTTGATCAGCCATGATGATACTTCTCGGAGAGAGCAAGGTGATGACAG 2496
QY 4628 GAGATCTGCGCCCGGCACTTCCGCCAATAGCAAGCCAGTCTTCCGCTTCACTGACAC 4687
DB 2495 GAGATCTGCGCCCGGCACTTCCGCCAATAGCAAGCCAGTCTTCCGCTTCACTGACAC 2436
QY 4688 GTGAGCAAGCTGCGCAAGAAAGCGCGTGGGCGAGCGAGTAAGCCGCGCTGCTC 4747
DB 2435 GTGAGCAAGCTGCGCAAGAAAGCGCGTGGGCGAGCGAGTAAGCCGCGCTGCTC 2376
QY 4748 GTCTGCACTTCACTTCAAGGCGACCGGACAGTCTGCTTGAAGAAAGCAAGCGCGCC 4807
DB 2375 GTCTGCACTTCACTTCAAGGCGACCGGACAGTCTGCTTGAAGAAAGCAAGCGCGCC 2316
QY 4808 CTGCGCTGACAGCGGAAACAGCGCGCATCAGAGCAAGCCGATTTGTTGTGCGCAATC 4867
DB 2315 CTGCGCTGACAGCGGAAACAGCGCGCATCAGAGCAAGCCGATTTGTTGTGCGCAATC 2256
QY 4868 ATAGCGGAATAGCTCTCCACCCAGCGCGGAGAACCTGCTGCAATCCATCTTGTTC 4927
DB 2255 ATAGCGGAATAGCTCTCCACCCAGCGCGGAGAACCTGCTGCAATCCATCTTGTTC 2196
QY 4928 AATCATGCGAAACGATCTCTCATCTCTCTTGTGATCAATCTTG 4971
DB 2195 AATCATGCGAAACGATCTCTCATCTCTCTTGTGATCAATCTTG 2152

RESULT 15
US-11-213-368-15/c
; Sequence 15, Application US/11213368
; Publication No. US20060003936A1
; GENERAL INFORMATION:
; APPLICANT: Mayerkuckuk, Phillip
; APPLICANT: Banerjee, Debabrata
; APPLICANT: Bertino, Joseph R.
; TITLE OF INVENTION: Method for Modulating the Production of a Selected
; TITLE OF INVENTION: Protein In
; FILE REFERENCE: MSK-P-053
; CURRENT APPLICATION NUMBER: US/11/213,368
; PRIOR FILING DATE: 2005-08-26
; PRIOR APPLICATION NUMBER: US/10/421,285
; PRIOR FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: US 60/375,250
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 4151
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cloning vector pGFP-L, complete sequence, enhanced
; OTHER INFORMATION: green
; OTHER INFORMATION: Fluorescent protein (egfp) and neomycin phosphotransferase genes
US-11-213-368-15

Query Match 29.7%; Score 1569.8; DB 17; Length 4151;

Best Local Similarity 86.3%; Pred. No. 0;
Matches 1847; Conservative 0; Mismatches 112; Indels 180; Gaps 3;
QY 3013 AAGGGGTAATACGTTATCCAGAAATCAGGGGTAACGAGAAAGAACTGTGACGA 3072
DB 4147 ATGGCGTAATACGTTATCCAGAAATCAGGGGTAACGAGAAAGAACTGTGACGA 4088
QY 3073 AAAGCCAGCAAAAGGCGAGGAACCGTAAGAAAGCGGGTGTGCGCTTTTCCATAGG 3132
DB 4087 AAAGCCAGCAAAAGGCGAGGAACCGTAAGAAAGCGGGTGTGCGCTTTTCCATAGG 4028
QY 3133 CTCGCCCCCTGAGAGACATCACAAAATCAGCGCTCAAGTCAAGGTGCGAAACCG 3192
DB 4027 CTCGCCCCCTGAGAGACATCACAAAATCAGCGCTCAAGTCAAGGTGCGAAACCG 3968
QY 3193 ACAAGACTAATAAGATACAGAGCGTTTCCCTTGAAGCTCCCTGCTGCTCTGTT 3252
DB 3967 ACAAGACTAATAAGATACAGAGCGTTTCCCTTGAAGCTCCCTGCTGCTCTGTT 3908
QY 3253 CCGACCTGCGCTTACCGGATACCTGTCGCGCTTTCCTTCCGCGGAAGGCGGCTT 3312
DB 3907 CCGACCTGCGCTTACCGGATACCTGTCGCGCTTTCCTTCCGCGGAAGGCGGCTT 3848
QY 3313 TCTCATAGCTCAGCTGATGATCTCAATTGCGGTGATAGTCTGCTCCAGCTGAGC 3372
DB 3847 TCTCATAGCTCAGCTGATGATCTCAATTGCGGTGATAGTCTGCTCCAGCTGAGC 3788
QY 3373 TGTGTGCAAGAACCCCGCTTCAAGCCGACCGCTGCGCTTATCCGTTACTATCTGCTT 3432
DB 3787 TGTGTGCAAGAACCCCGCTTCAAGCCGACCGCTGCGCTTATCCGTTACTATCTGCTT 3728
QY 3433 GAGTCCAAACCGGTAAGACAGACTTATCCGACCTGCGAGAGCACTGTAACAGATT 3492
DB 3727 GAGTCCAAACCGGTAAGACAGACTTATCCGACCTGCGAGAGCACTGTAACAGATT 3668
QY 3493 AGCAGAGGATATGTAAGCGGTGCTACAGAGTCTTGAAGTGTGAGCTTAACAGC 3552
DB 3667 AGCAGAGGATATGTAAGCGGTGCTACAGAGTCTTGAAGTGTGAGCTTAACAGC 3608
QY 3553 TACACTAGAAAGACAGATTTTGTATCTGCGCTCTGCTGAAGCAGTTACTTGGAAA 3612
DB 3607 TACACTAGAAAGACAGATTTTGTATCTGCGCTCTGCTGAAGCAGTTACTTGGAAA 3548
QY 3613 AGATGTTAGCTCTTATATCCGCAACAAACCGCTGTAGCGGTGTTTTTGT 3672
DB 3547 AGATGTTAGCTCTTATATCCGCAACAAACCGCTGTAGCGGTGTTTTTGT 3488
QY 3673 TGCAGAGCAGATTTACGCGCAAGAAAGATCTCAAGAGATCTTGTATCTTCT 3732
DB 3487 TGCAGAGCAGATTTACGCGCAAGAAAGATCTCAAGAGATCTTGTATCTTCT 3428
QY 3733 ACGGGTCTGACGCTCAGTGAACGAAACTCAGCTTAAGGATTTTGTGATGATTA 3792
DB 3427 ACGGGTCTGACGCTCAGTGAACGAAACTCAGCTTAAGGATTTTGTGATGATTA 3368
QY 3793 TCGTGCAGCAAAAGCGGCATCTGCCC----- 3819
DB 3367 TCAAAAAGATCTTCACTAGATCTTTTAATTAATTAAGATTTTAATCAATCTAA 3308
QY 3820 -----CCCCACTCTGCACTTCCGGGGCATG 3845
DB 3307 AGTATATATAGTAAGTACCTGAGGCTATAGGACAGGCTCCGCCCGAGAGTTGCTGCAAGC 3248
QY 3846 GATGCGGATPAGCCGCTGCTGTTCTGATATGCGACGATTTGACTCCGG----- 3900
DB 3247 CTGCGGCTTCACTCGAACTTGGGGGGTGGGGTGGGAAAGAAAGCAAGCGGGCTAT 3188
QY 3901 -----TAGAACTCCGAGAGTGTCTCAGGCTCAGGAGCAAGCTCAACTGCG 3951
DB 3187 TGGCCCCAATGGGGTCTGGGTGGGTATGACAGAGTGCAGGCCCTGGAGCAAGACCCG 3128
QY 3952 AGGAGATCGA----- 3961

Db 3127 CGTTTATGAACAACGACCAACGCGTTTATTCTGTCTTTTATTGCCGTATA 3068
QY 3962 -----GCCGGGGTGG 3972
Db 3067 GCGCGGGTTCCTTCGGTATGTCTCCTCCGTGTTCAGTAGCTCCCTTAGGGTGG 3008
QY 3973 GCGAAGAACTCCAGCATGAGATCCCGGCGCTGAGAGATCATCCAGCGGCGTCCGGAAA 4032
Db 3007 GCGAAGAACTCCAGCATGAGATCCCGGCGCTGAGAGATCATCCAGCGGCGTCCGGAAA 2948
QY 4033 ACGATTCCGAAGCCCAACTTTCATAGAGCGCGGTGGAATCGAATCTGTATGGC 4092
Db 2947 ACGATTCCGAAGCCCAACTTTCATAGAGCGCGGTGGAATCGAATCTGTATGGC 2888
QY 4093 AGGTTGGGCGTCCGTGTTGGTGGTCTATTCCAACTCCGATGCCGCTCAGAGAACTGT 4152
Db 2887 AGGTTGGGCGTCCGTGTTGGTGGTCTATTCCAACTCCGATGCCGCTCAGAGAACTGT 2828
QY 4153 CAAGAAAGCGATAGAGAGCGATGGCGCTGCCAATCGGAGCGGAGTAACCGTAAAGCACA 4212
Db 2827 CAAGAAAGCGATAGAGAGCGATGGCGCTGCCAATCGGAGCGGAGTAACCGTAAAGCACA 2768
QY 4213 GGAAGCGGTCAAGCCATTTCGCGCCAAAGCTCTTCAGCAATATCACGGGTAGCCAACTGA 4272
Db 2767 GGAAGCGGTCAAGCCATTTCGCGCCAAAGCTCTTCAGCAATATCACGGGTAGCCAACTGA 2708
QY 4273 TGTCTGTATGCGGTCCGCCACACCCAGCGGCCACAGTGAATCCAGAAAAGCGGC 4332
Db 2707 TGTCTGTATGCGGTCCGCCACACCCAGCGGCCACAGTGAATCCAGAAAAGCGGC 2648
QY 4333 CATTTTCCACCATGATATTTGGGCAAGAGGAGATGCCATGGGTCAAGACGAGATCCTCGC 4392
Db 2647 CATTTTCCACCATGATATTTGGGCAAGAGGAGATGCCATGGGTCAAGACGAGATCCTCGC 2588
QY 4393 CGTGGGCGATGCGGCGCTTGAAGCTGGCGAAAGTTGCGTGGCGCGAGCCCTGATGCT 4452
Db 2587 CGTGGGCGATGCGGCGCTTGAAGCTGGCGAAAGTTGCGTGGCGCGAGCCCTGATGCT 2528
QY 4453 CTTGCTCCAGATCATCTGTATCCAGACACCGGCTTCCATCCGAGTACGTGCTCGTCCA 4512
Db 2527 CTTGCTCCAGATCATCTGTATCCAGACACCGGCTTCCATCCGAGTACGTGCTCGTCCA 2468
QY 4513 TGCATGTTTTCGCTTGGTGGTGCATGGGAGGTAAGCCGGAATCAAGCGTATGACCGCC 4572
Db 2467 TGCATGTTTTCGCTTGGTGGTGCATGGGAGGTAAGCCGGAATCAAGCGTATGACCGCC 2408
QY 4573 GCATTGTCATCAGCCATGATGATATCTTCTCGGACAGGCAAGGTGATGACAGAGAT 4632
Db 2407 GCATTGTCATCAGCCATGATGATATCTTCTCGGACAGGCAAGGTGATGACAGAGAT 2348
QY 4633 CTGCCCCCGGCACTTCCGCCAATAGCAGCAATGCCCTTCCGCTTCAGTGAACAAGTCCA 4692
Db 2347 CTGCCCCCGGCACTTCCGCCAATAGCAGCAATGCCCTTCCGCTTCAGTGAACAAGTCCA 2288
QY 4693 GCACAGCTGCGAAGAAAGCCCGTGTGGCCAGCCAGATAGCCGCGCTGCTGCT 4752
Db 2287 GCACAGCTGCGAAGAAAGCCCGTGTGGCCAGCCAGATAGCCGCGCTGCTGCT 2228
QY 4753 GCAGTTCAATCAGGGGCAACCGGACAGGTGCTTTGACAAAAGAAACCGGCGCCCTGCG 4812
Db 2227 GCAGTTCAATCAGGGGCAACCGGACAGGTGCTTTGACAAAAGAAACCGGCGCCCTGCG 2168
QY 4813 CTGACAGCCCGGAAACACGCGCGGCATCAGAGCAGCCGATTTGTGTGTGCCAGTCATAGC 4872
Db 2167 CTGACAGCCCGGAAACACGCGCGGCATCAGAGCAGCCGATTTGTGTGTGCCAGTCATAGC 2108
QY 4873 CGAATAGCTCTCTCAACCCAGCGCGGAGAACTGCGTGAATCCATCTTGTTCATCA 4932
Db 2107 CGAATAGCTCTCTCAACCCAGCGCGGAGAACTGCGTGAATCCATCTTGTTCATCA 2048
QY 4933 TGCAGAAAGATCTCATCTGTCTCTTGTGATCAGATCTTG 4971
Db 2047 TGCAGAAAGATCTCATCTGTCTCTTGTGATCAGATCTTTG 2009

Search completed: May 14, 2006, 08:40:20
Job time : 1502 secs